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AF155804 Streptogoccus suis strain 6555 Cps1E (cps1E) gene, partial cds; Cps2F (cps2F), Cps1G (cps1G), Cps1H (cps1H), Cps1I (cps1I), and Cps1J (cps1J) genes, complete cds; and Cps1K (cps1K) gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-UUN-1999) Bacteriology, Animal Science and Health, P.O. Box 65, Lelystad 8200 AB, The Netherlands Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, H.B., Damman, M., van der Velde, J., Wagenaar, F., Wissellink, H.J., Stockhofe-Zurwieden, N. and Smits, M.A. Identification and characterization of the cps locus of Streptococcus suis serotype 2: the capsule protects against phagocytosis and is an important virulence factor Infect. Immun. 67 (4), 1750-1756 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus suis
Streptococcus suis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Smith, H.E., Veenbergen, V., van der Velde, J., Damman, M.,
Wisselink, H.J. and Smits, M.A.
The cps genes of Streptococcus suis serotypes 1, 2, and
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Smith.H.E., Veenbergen,V., Van der Velde,J., Damman,M.,
Wisselink,H.J. and Smits,M.A.
Direct Submission
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/mol_type="genomic DNA"
/strain="6555"
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AX083715 Streptoco
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AZ88961 Streptoco
X85787 S.pneumonia
AY376403 Streptoco
AF04245 Streptoco
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KKL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ATTATTTTGCATTTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAAGTCATATACCAAATGCTGATTTAAATCGTTCTGGAATTTTTATCATAATGATGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TAGAGTTTGAAAAACATTTAACTATAGTATAATTATTGCAATTTTTCTTACGGCAGTAT
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I YI EVPDRVNKSTLTGKLVYPVTDI FI VQWEEMKKVYPKS I NLGSI F"
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                                                                                                                               Streptococcus suis Cps2A (cps2A), Cps2B (cps2B), Cps2C (cps2C), Cps2D (cps2D), Cps2E (cps2E), Cps2C (cps2C), (cps2B), Cps2F (cps2F), Cps2G (cps2), Cps2H (cps2F), Cps2E (cps2H), Cps2I (cps2I), and Cps2I (cps2I) genes, complete cds; AF118389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-JAN-1999) Department of Bacteriology, DLO-Institute for Animal Science and Health, P.O. Box 65, Lelystad 8200 AB, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus.

1 (Bases 1 to 15401)

Wisselink,H.E., Damman,M., van der Velde,J., Wagenaar,F.,
Wisselink,H.J., Stockhofe-Zurwieden,N. and Smits,M.A.
Identification and characterization of the cps locus of
Streptococcus suis serotype 2: the capsule protects against
Dhagocytosis and is an important virulence factor
Infect. Immun. 67 (4), 1750-1756 (1999)
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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Smith, H.B., Damman, M., van der Velde, J., Wagenaar, F.,
Wisselink, H.J., Stockhofe-Zurwieden, N. and Smits, M.A.
Direct Submission
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SOURCE
ORGANISM
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                                                           ATTITITICACTAATCATAGTGGAGTATCAAATGCTAGAAATCATGGAATAAAGCGGAGT
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TTAVLEGIYLKRKLKLPLLMHVHEIIVKPKFISDSINFLMGRFADKIVTVSQAVANHI
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codon start=1
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Best Local Similarity
Matches 1437; Conserv
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14781 TCAGATGCCCGTAATTATGGCATAAGTCGCGCCAAGGGTGACTACTTAGCTTTTATAGAC 14840
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AY057915.1 GI:24473733
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                                            TCAGATGATTTTATTCATTCGGAGTTCATCCAACGTTTACACGAAGCAATTGAGAGAG
                                                                                                                                  6492 AATGCCCTTGTGGCAGTTGCTGGTTATGATAGGGTAGATGCTTCGGGGCATTTCTTAACA
                                                                                                                                                                                                                          GCAGAGCCGCTTCCTACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTG
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Streptococcus thermophilus
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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1 (bases 1 to 17468)
Rallu,F., Ehrlich,D.S. and Renault,P.
Diversity of eps operons in Streptococcus thermophilus Unpublished

    .17468
    ^organism="Streptococcus thermophilus"
/mol_type="genomic DNA"
    /db_xref="taxon:1308"

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Rallu,F., Ehrlich,D.S. and Renault,P.
Direct Submission
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<1. .492
/gene="deoD"
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SOURCE
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                                                                                                                            /protein_id="AAL23730.1"

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/db_
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VYIEVFDRIDKPTVTGKLVYPVTDKFIVQWFERKKVYPKAINLGSIF"
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HQVDFARNVAKRMGTIILVEDVDKLGETIENYNSIVAELBYDMGNNNKKFNKDLEGIV
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note="undecaprenylphosphate glucosyltransferase"
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|genc="eps3G"
|note="putative galactosyltransferase enhancer"
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/gene="eps3F"
/note="Eps3F; putative undecaprenylphosphate
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pseudo
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/pseudo
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6275. .7647
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/gene="eps3G"
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/product="eps3H"
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product="Eps3E"
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product="Eps31"
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trans1 table=
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/gene="orf3A"
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gene="orf3A"
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/gene="eps3H"
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KNNKEI DLFFEENKGKEFILYDNNTLEDNLEI SRRTKYYHFLONYRRRYTENWKNSFF
TFCERVSLVLOI I FGVNRVKNLDWOI KYGSOWVSITNELVKTI LEHEEKITSI FQYTK
CKNHREDSI FISFNSQVSNN"
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ps Partent: WO 0179500-A 9 25-OCT-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
COMPAGNIE GERVAIS-DANONE (FR); Rhodia Chimie (FR) chaattiteleagigetelegijgalaagititeateaatgagiaaattiaigaaa 8021 CCAACAGTTACAGGAAAATTAGTGTACCCTGTGACGGATAAGTTCATTGTTCAATGGGAA GAGATGAAAAAGTTTATCCAAAAGCTATTAATTTAGGGAGTATCTTTTAATGATTTTG TAACAGTAGGAACACGAACAACCTTTTAATCGCTTAATTCAGGAAGTGGATCATTAG GAAAAAAACAATTATTGTTTCCTAGACAAAAAAGTATGGTGAACATGTAAATGATCATC 3381 GCAAAAAGCCAATTGTTGTCCCTAGACAAAAAGTTTGGTGAACATGTCAATGACCATC *LTTAATGATTTTTG* 1893 AAAAAAATGGAAGTATAACCGACGAAATATTTATTCAAACAGGATATTCTGACTATATTC CAGAATATTGCAAGTATAAAAATTTCTCAGTTACAAAGAAATGGAACAATATAAACA AATCAGAAGTAGTTATTTGCCACGGAGGCCCCCGCTACTTTATGAATTCATTATCCAAAG <u> Aagcrgatattattatcacrcacgaggrccagcgactrttatgagrgccattacaarg</u> 1 ATCGCCAAACGAAATTGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAA 41; Gaps Streptococcus thermophilus Streptococcus thermophilus Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, PAT Length 17468; Indels linear GAAATGAAGAAGGTATATCCTAAATCTATTAACTTGGGGAGTATTT 1. .17468 /organism="Streptococcus thermophilus" /mol_type="unassigned DNA" /db_xref="taxon:1308" Query Match 13.7%; Score 955.6; DB 6; Best Local Similarity 65.8%; Pred. No. 6.2e-99; Matches 1484; Conservative 0; Mismatches 729;

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BQFYPCYFPTNRNFKNLVKNTFLALKILRKERPDVIISSGAAVAVPFFYLGKLFGAKT
VYIEVFDRIDKPTVTGKLVYPVTDKFIVQMEEMKTVYPKAINLGSIF"
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QYCDWKNIISYPEMEDYMNRADIIITHGGPATFMGAIAKGKKPIVVPRQEKFGEHVND
HQLDFAYQVKDRYDNIEVVEDIKTLQQFLKQDLSISESTTSNNKKFNEQLRQEVENIM
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/db_xref="G1:18076396"
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function="glycosyltransferase"
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/evidence=not_experimental
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/Jene="eps1"
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/evidence=not_experimental
/transl_table=11
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/gene="eps3"
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/gene="eps4"
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/gene="eps1"
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Xolkman,M.A., van der Zeijst,B.A. and Nuijten,P.J. Functional analysis of glycosyltransferases encoded by the capsular polysaccharide biosynthesis locus of Streptococcus pneumoniae
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                                Kolkman,M.A., Morrison,D.A., Van Der Zeijst,B.A. and Nuijten,P.J. The capsule polysaccharide synthesis locus of streptococcus pneumoniae serotype 14: Identification of the glycosyl transferase
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Submitted (23-APR-1996) M.A.B. Kolkman, Institute of Infectious
Diseases and, Immunology, Department of Bacteriology, School of
Veterinary Medicine, University of Utrecht, P.O. Box 80.165, NL
-3508 TD Utrecht, NETHERLANDS
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Submitted (16-JUN-1997) M.A.B. Kolkman, Institute of Infectious
Submitted (16-JUN-1997) M.A.B. Kolkman, Institute of Infectious
Submitted and, Immunology, Department of Bacteriology, School of
Diseases and, Immunology, Department of Urecht, P.O. Box 80.165, NL
-3508 TD Utrecht, NETHERLANDS
On Jun 17, 1997 this sequence version replaced gi:1279732.
Location/Qualifiers
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J. Biol. Chem. 272 (31), 19502-19508 (1997)
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/function="degradation of glucans
/codon start=3
/rransl_table=11
/product="alpha, 1-6-glucosidase"
                                                                                                                                                                            J. Bacteriol. 178 (13), 3736-3741 (1996)
96272244
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/isolate="NCTC 11902"
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/sub_clone="cMK02"
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7 (bases 1 to 14943)
Kolkman,M.A.B.
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5 (bases 1 to 1821)
Kolkman, M.A.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 14-JUL-2000
                                                                                                                                           1634 TGCTGTCCCCTTCTTTACATCGGAAAACTATTTGGAGCAAAGACGATTTATATTGAAGT 1693
                                                                                                                                                                                                                                                                                      ATTTGATCGAGTTAATAAATCTACATTAACTGGAAAACTAGTTTATCCCGTAACAGATAT 1753
                                                                                                                                                                                                                                                                                                                                                    ATTTGATAGATAGATAAACCGACAGTAACTGGGAAATTGGTTTATCCAGTGACAGATAA 8527
                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTATTGTTCAGTGGGAAGAAATGAAGAAGGTATATCCTAAATCTATAACTTGGGGAG 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8528 ATTTATTGTTCAGTGGGAGGAGATGAAAACTGTCTATCCCAAAGCTATTAATCTGGGGAG 8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTTTTAATGATTTTTGTAACAGTAGGAACTCATGAACAACAGTTTAATCGATTGATA 1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8588 TATTTTTAATGATTTTTGTTACAGTGGGAACCCACGAACAGCCCTTTAATAGGCTTATT 8647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8648 AAGGAAGTTGATCGTTTAAAAAAGAAGGTATTATTACAGATGAGGTTTTTATTCAGACA 8707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATATTCTGACTATATTCCAGAATATTGCAAGTATAAAAAATTTCTCAGTTACAAAGAA 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8708 GGTTTTTCAACTTATGAACCTCAATACTGTGACAAGAAAACATTATTCTTATCCTGAA 8767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1994 ATGGAACAATATATAACAAATCAGAAGTAGTTATTTGCCACGGAGGCCCCGGTACTTTT 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8768 AriddaAdarrahárdaArcgrecadararrahárdacgcardcrecededacarre 8827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8828 ATGGGAGCAATTGCTAAAGGAAAAAACCGATTGTTGTTCCAAGACAGGAAAAGTTTGGA 8887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cps14E gene;
cps14J gene;
       AGCTTTCAAAATTTTACGTGATGAGAAACCAGATGTTATTATTTCATCTGGTGCGGCCGT
                                               cosida gene; cosida gene; cps14C gene; cps14D gene; cps14E cps14F gene; cps14G gene; cps14G gene; cps14d gene; cps14d gene; cps14c gene; cps14L gene; cps14E gene; cps14E gene; cps14E gene; cps14E gene; cps14E gene; cps14E gene; cps14D gene
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Streptococcus preumoniae
Streptococcus prantoneumoniae
Bactestia, Firmionteumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9127 AATTACATCAAGTGTTATTTCTATGAAGTTTTAAGTATATA 9167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss-1,4-galactosyltransferase; tasA gene.
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ACCESSION
VERSION
KEYWORDS
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SPCPS14E
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/trānslation="MKEONTLEIDVLQLSRALMKRKLVILLVAIITSSVAFAYSTFVI
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LTFRGLANKT KVTVPVDTRIVSVSVNDRVPEEASRIANSLREVAAQKIISITRVSDVT
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DAVIITOKDASILVTATGEANKRDVQKAKQQLEQTGKLFLGVVLNKLDISVDKYGVY
ASYGNYGKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5275 AACGGTTTAGTATCTCTAGAAGAAGGAATGGTATACTTCTTAACTTTAGAAGGAATATCCT 5334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5395 Atagcaagaaatttttachgrtaacagtaacggaaatatagaaaagttcttgataaat 5454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="capsular polysaccharide synthesis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 TATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTCGACAATCT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5215 CTATAAGATATATTTTTTTTTTGCAATAGCTATAAGTGTATTAAACTTTTTTATAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 ATCAAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCTGATTTAAATCGTTCTGGAATTTTTATCATAATGATGGTTCATTATTTTGCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5095 AGACAGAACTTGAACGTTCTTCGATGGTTATACTATACCTTCTCCCACTTTTTTTGTATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 TTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 CATTTAACTATAGTATAATATTTGCAATTTTTCTTACGGCAGTATCATTTTTGTTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 ATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/db_xref="GG1:1279735"
/db_xref="GGA:P72512"
/db_xref="UniProt/TrEMBL:P72512"
                                                                                                                                                                                                                                                                                                                                                                                 function="putative polysaccharide export protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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Pred. No. 4.9e-91;
0; Mismatches 859;
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                                                                                                                                                                                                                                                                                                                                                                                                                               table=11
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4995. .5000
                                                                                                                                                                                                                                                               /gene="cps14D"
4308. .4991
                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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5007. .6374
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62.7%;
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Best Local Similarity 62.7°
Matches 1482; Conservative
                                                                                                                                                                                                                                                                                                                                      1308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGMFETPEEKIAENFLQVREIAKEVADDLVIAYGAEIYYTLDALEKLEKKEIFTLNDS
SYALIEKSWHTTSYROHTGAESNILMLGITPVIAHIERYDALENNEKHVRELIDMGCYT
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EFSALHGKFHPPVGNVHLDSEQALGFVRERYSLADGDRDRGRNQQKVIVAILQKLTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EALKNYSTIIDSLQDSIQTNMPLETMINLVNTQLESGGNYKVNSQDLKGTGRTDLPSY
AMPDSNLYVMEIDDSSLAVVKAAIQDVMEGR"
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408. .1410
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                                                                                                                                                        700. .753
join(1054.
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-35_signal
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/product="capsular polysaccharide synthesis protein"

Db 6550 ATCANGTHYNIACCACAACCAACCAACCAACCAACCAACCAACCAACCA	RESULT 7 AY376403 LOCUS LOCUS DEFINITION Streptococcus agalactiae strain 7271 Cps7C, Cps7D, Cps7E, Cps7F, Cps7C, Cps7H, Cps7M, Cps7I, Cps7Z, Cps7L, NeuB, NeuC, NeuD, and NeuA genes, complete cds. ACCESSION AY376403 KEYWORDS Streptococcus agalactiae ORGANISM Streptococcus agalactiae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
135 TICANTCACHINACAMITCANAMATICTICATRICATRICATRICATRICATRIAN 195 545 FOCTGANCTICATRICANCAL TECHNOLOGY CONTROL	1336 AAGTTGTATTGTGAGGAGGAGGTAAAGTAAAAGTTTGAAAGTTTGGTGG

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                      Cieslewicz, M.J., Glusman, G., Chaffin, D., Kasper, D., Madan, A., Acdrigues, S., Fahey, J., Wessels, M.R. and Rubens, C.B.
Byolution of group B Streptococcus capsular polysaccharides
Unpublished
2 (bases) to 14202)
2 (bases) to 14202)
Cieslewicz, M.J., Madan, A., Wessels, M.R., Kasper, D. and Glusman, G. Direct Submission
Direct Submission
Submitted (28-Ad07-2003) Channing Laboratory, Brigham and Women's Hospital, 181 Longwood Ave, Boston, MA 02115, USA
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GTAATGGTAGGATTTTTAGATTCTATAAATTCAGATCAATGCGAGTAGATGCAGAACAAA
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                                                                                          --- ACGACCATAATTATATCGCTGTCTGTATCTTGGACTCCTCTGAAAGG
                                                                                                                              AAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT
                                                                                                                                                                  ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG
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                                             /translation="MATTKALLOSGFITTIGNLLUOGIAFITLDFITTRVISTEVYGOVS
LIVVAMMGIIALPIGLOTSGSLSSARVKYGEEPKSYSGSAFSVGNIWFLLIVLLVAFLFR
STADENUGRESESIFLLANICOSYANIVYTFGOTTOGORSFANLLISELTIANYSSVALS
LFLIFHWSDDFLSRYCGAFVDFILIVALVAFFGOTYXTSKSFYNSKYFRFITNYSSVALS
LFLIFHWSDDFLSRYCGAFVDFILIVALVAFFGOTYXTSKSFYNSKYFRFITNYSSVELIF
HLLGHOLLNOLDRIMLARLYNTKEVAMYSFGYSLGMIIQIVANSINNAMIPWFFDARK
AKLLOLPTYSTSKYLKYFTGVFLTGYLTFFDELAQIMGGDKYSSSVQFISLIIVSYFLVF
LYTFPVNIQFFYANTTWIPIGTLLAAGVNWLLMLVLIPNYAAYGAMATVISYLALI
FHHIVSKYKYHTLUDKYSRQYILLSGIVFSYAMLMNWFLDNIVVRWGLGIMILIVYSIV
                                                                                                                                                                                                                                                                                                                                             /translation="MVYIIAEIGCNHNGDINLAKKMVDVAVSCGVDAVKFQTFKAEKL
ISKFAPKAEYQKATTGTADSQLEMTKKLELSFEEYLEIRDYALSKGVETFSTPFDEES
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TTDISTLHCTTEYPPTSAINLAVVITHLKDEFKDLTIGYSDHSIGSEVPIAAAAIGAE
YIEKHPTLDTRMEGPDHRASATPDILAALVKGYRIVEQALGREPKIPDPVEEKNKIVA
RKSVVALKPIKKGDIYSIENITVKRPGNGISPMWYDILGQEAQDDFEEDEVIRDSRF
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YRYTRQIBEDGFDIATKUPKPLHALVTDRRTVEYTHAHQLGITKTRERBEYDLUTILG
YRYBKLEVNAVVALI YNVPVCHLHGGFTSLGRFDBYIRHAITKMSHLHLVSTEDFRQNE
IQMGEQPQFVINTGALGVENALSIPSLIYERAIEKQLGIVLEESYFVVLYHPVTFEQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGEQMKAVLSALSKFGVQCLPIGSNSDTGSDDIAKAINTYLINHENSYCFASLSTQL
YHSLIRHSLGLIGNSSSGLIEVPSLMKPTLNIGDRQKGRLHGESVVSVPVETSSVLRG
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Pred. No. 7.3e-86;
                                                                                                                                                                                                                                                                                           'product="NeuB"
'protein_id="AAR25956.1"
'db_xref="GI:38640645"
                /protein_id="AAR25955.1"
/db_xref="GI:38640644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAR25957.1"
db_xref="GI:38640646"
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4922 4685 GGAAAİAGTTTTAAGGAAACAAGİGİCCİGTİTĞAİAAİAGCTACİÇİATGİTA--TIGA 4742 4923 GIGATGGIATTGAACCAATAAAAAGAATTTACTATTATAGACGATATATGATATATTT 4982 2684 GIICTAATIGGGIITICGCIICCACAIGAITITIGIGGCAATICTITITATCAAATGAAAACG 2743 4385 AAGCTTATTGTAATAGTTTTATTTTTAAGATTATTTACTGTATCAATATACTTTT 4444 2858 TAAAGTGGAAAAATCAACATCTTCTCCTATTGTCTTTACAGATGATTCTATTGATGAAT 2917 3038 GITTAAATTATTTAAATATGACCCGGAATATTTTTATTTTTAAGTACTTCTGGTTGATTAT 3097 4625 cirirgacaggiaggriaaacrargcrcarriacaacriggragacggrrigacrcrrrrr 4684 3158 TATAAAATTTTTGAAAACTAAGCTAATATTAAAAATGAAATTTTATTGTTTTATTATG 3217 4743 GTATGTATGGTGTAGTCCTTACCCTGTTTTGATGATAATCTATTATGTTTACAGTAAAG 4802 4803 AAATAAGAATACTTGAACTTCAATTACTGCTATTTATAATGTCTATAGTATTATTACAG 4862 3278 ATTATTTGCAGATTTTACTGCTCCCATAATTTGGATTATTGCAATAATGTATTATAATTT 3337 3338 GTATTCATTTATAAATATGATTATAAAAATTAAAAAATAGTATCTTTTTTAGTTTTTT 3397 3398 AGTITIAITAGGIATATCTGCAITGIATATTATTCAAAATGGGAAAGATATTGTATTTT 3457 4983 ATTCTGATATAGTAGGATGTGAGGAAACAAATGATACCTAAAGTTATACATTATTGTTGG 5042 5043 TTTGGAGGAAATCCCTTACCTGATAATTTAAAAAGTACATAAAAACCTGGAGAGAACAA 5102 3518 CTTTATGAACTATCCTACGTTAAATACCACTACAATTATAGTTTCAATTCCGTTAATCTT 3577 3578 IGCACTIATAAAAATAAAAIGCAACAATITITITITITIGIGICITIGCTITITAAAAAA 3637 5163 TTTATGAGAGAATATACTAAGAAAAATTTTGCCTATGTTTCTGATTATGCAAGGTTG 5222 4265 THTTATAGAGATGGACATTTCATTCTGAGAAGTGACTTAGGTTTTGGGGATCCCAACTTT 4324 2744 AAACAGCTTATTTATTTAAGTAATCTAAATGTCCAGATGAACTATTTATACAGACAATTA 2803 4325 ATTCATAATTTTTTTGCTCTAACCTTTTTTTTTGTATTGTACTCAATTATAAACGACTG 4384 2804 TAGAAAATATGAATTTTCAAATAGATTATCTAAATATGGAAATTTAAGA-----TATA 2857 4145 GCATTGAAGGATATCTCTCTAAAAAGCTTTCTCTATAATAATAAGGATCGCGTATATTG 4204 4565 riracririrricakorricracaarrrrrrrcaarrcaaarrricriccaaaarragaraak 4624 2564 AAAACTATTGATAATGTACTGTTTAGAATTTTTAATAAGAATGTATCGAGCTTTTTGAATAC 4445 icaadaacagggaatatatatataaittiaittatigtactcaittaictaacaagaat 2624 TATTTACAAAGATTGTTTATTGATAGAATAAAAAACATGGTCTAAGAATAAGATTTG 4205 GGAGTTCTATTAAATCAAATTTTGTGAAATTAGATTTTGTAGAAATAAAGTATGTCAAT 4863 AGAGTITITACCCAAGTATAGTATATTAGTTAGTTAGTTAGTTTTGGGAAAATATTT

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VLPVQFFLLVYPTFLSSTIFPNSNPVQKLDVLLTGRLHYAHLQLVDGIPFFGNSFKETS
VLPNNSYSMLLSMYGVVLTMFCMIIYYTYSKKIIIIBLQLLLFIMSIILFTSFFPSV
VMNISWLLSMYGVVLTMFCMIIYYTSKKIIIIBLQLLLFIMSIILFTSFFPSV
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HQVDFVNKVKTMYNFDIVVDIERLQNVVYEGMMNRPFLETNSSNFIEEPKVILKELCD
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                                                                                        note="beta-1,4-galactosyltransferase"
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3762. .9649

'gene="cp8VN"

'note="putative glycosyltransferase"

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Pred. No. 2.6e-81;
0; Mismatches 3382;
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8001. .8006
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8011. .8736
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5255 5435 9916 5495 9266 5555 5615 4595 4715 4775 4835 4955 5015 5075 5135 5195 9736 5315 5375 9213 4895 9387 9447 9616 9271 9331 9448 AAATTCATATATGTATGTAATGTCTTTTTCCTAATATATTTGATCGCTGGTGGTCAGC--T 9505 9506 ATAAAGATAAAATGAACATACAGGCTTTGAAATGACTACTTTAGGGGTAATACCTACA 9565 TATCAGAATTTAGAGATTATCATTGATGATGGCCTCTAGTGATCGCCACAGGGGATATT 9796 TCCGAAAAGTATTTTTTGGAAGACAGGCGAATAAAATATTTCTATCAAGAAAACAGAGGC 9856 GACAGTGATGATGTTTATCTTCCTTATTCAATTGAGGTTATGTACAACATACAGAAAGCT GACTCTGATGATGTTGATAGTAGATTAGTAGAAAAATTATATTTTAATATATAAAA GAAGTGAATAATCCAAATATTGATTTTGAAGCAATTAATACCGTGCGGGACATGGGAGAA TAGATATGTAGGCCT----TGTTTATCCTCGATATTCATTAAACCAAGGTAATAG 4776 AACACGTGTAGTTGATACTAGAGAATATTATTATAATTATGTCATTCGTAACAGTTC 3388 GACTICIAATATITITAAATTATGGAGAAAAATTICAAAGGGACTATTTTTATAGA 5076 ATCAAGAAAGCATTTAGTTACGTTGTATTTTGATGAAATTTTCGCCTAAACTATATGTAAT CCAGTITATAATGTAGATAAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAAAT 9677 cergiarahangagaaararahananggagargichagaratricrigageaaacr 4536 AGCAGAGATAGATTTTTTGTTTAGTAGAAAAACGGGTATACAAAGAAAAAAGAAATAG 9040 GTTATTAGAAGATGCAGTTGAAATTATTTAAAGATTTAGAGAGCCTAACGTTGTCTAA TAATTTTCATGTCTTAACGAGAGAGAGACTGTAAAAGAATTTTTGTCAGGATCTAATAT 1656 AGAAAATAATGTTTGGTGCAAGCTTTATTCACGAGATATTAAAAAAGATATAAAAATTCCA 9154 GTTGAATCCCAAAATATTAGAAGTTAATATTCCTGATTTAAAATATAAATATATCACTTAAA AATTAATAATAGAAGTATTGGTGAGGATTTTGCTTTTTAATTTGGAGGTCTTGAACAATGT 9214 AATTGAAACTTGTATTGTTAATAA--TGCTTATTTAGTAGATTTCGAATTTCCTTGT GCTTATTAATCAGAAATTCTCTATAAATAATAATTGATTTAGTCACAAGATTGGAGAATTA 9332 TACTTTTGTCCCCAAAATAGGAAAATCTATTG----TTTTGACTACTTAGAAGATGGTTT 4956 GGTTAAATGTTTAAACAAAATGTATTCAACAGATTGTTTGGATAATGAGTTCTTGCCAAT ATTAGAGTCTTATCGAAAAGAAATACGTAGATATCCATTTATTAAAGCGAAAAGATATTT CTAAAG-----AGTGAAGAGGCTGGGTGGAAATTTTGTTGGGTTTTTAGCTATCTT 5136 GTTATATATAGAAATTTCAAAAGCAGTAGAGGTAAAAATGGATAAAATTAGTTATTGTT TATAAAAATATAGAAATATTATTGATAGATGATGGCTCTGTAGATGATTCTGCTAAAATA TGCAAGGAATATGCAGAAAAAGATAAAAGAGTAAAAATTTTTTTCACTAATCATAGTGGA AGTAGAAGTGATTTATCTGGTTGTTTGTACGCTACTTTTTCAGAAAATATAAATTTTT accaargccgararrgrinnaacragrarrggraacricaacaaracrracaaracragr 4596 9100 4716 4896 5016 5196 5256 9737 5316 7616 5436 9917 5496 5556

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                                                              ATGTATTATGGGAAAACTTATGGAGTTTCCCCGTTAGCAA----AATTATATCCGAGAA 10151
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                                                                                                                            GTAATTTATTGAGTAATCCATATCCAGAAGGAAAATTCATGAAGATATGGATACAACTT
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                                                                                                                                                                                                                            TITIATAGGAGAGGTATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCAA
                                                                                                                                                                                                                                                           10272 ATTTTAGCGATAATAGTACTACTAGGACAAAATTCAATGAGAGAATGT-TGTATTTTTT
                                                                                                                                                                                                                                                                                            5856 TTGGAAAATTTGCAAAAACAAGTGATAGTATTGTTTAAGCAAATATATGGTGAGGAJTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6567 ACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11040 GAAACTATTAGTCCAGTACAAGCAATACAAAATATTTATAAA---TTATGATGCCTATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6627 CATCGCTTTGTGGTGGCCTGTAATAAACTCTATAAAAAGAACTATTTGAAGATTTTTCGA
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11157 TATCCAGTAGGGAAGTTACACGAAGATGAATTTTTAACCTATAAATTATATTTGAAAGCC 11216
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1 (Dages 1 to 21365)
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Peterson, S., Wessels, M.R., Paulsen, I.T., Nelson, K.E., Margarit, I.,
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Khouri, H., Mulligan, S., Carty, H.A., Cline, R.T., Gill, J.,
Scarcelli, M., Wora, M., Iaoobini, E.T., Brettoni, C., Galli, G.,
Mariani, M., Vegni, F., Maione, D., Rinaudo, D., Rappouli, R.,
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Complete genome sequence and comparative genomic analysis of an
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TTTGAAAAGGGTAAGATTCATGAAGATGAATACTTCACTTATCGCTTGCTCTATGAGTTA
                                                                                                                                                                                    GAAAAAGTTGCAATAGTTAAGGAGTGCTTGTACTATTATGTTGACCGAGAAAATAGTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             11277 Argáchggtrccracaararraaaaggcracargcrgragaagcacrraa 11326
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protein id="AAN00043.1"
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Streptococcus agalactiae 2603V/R
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                        ACAACTICTAGCATGACTGACCATCGCTTCCATTGCCTACTGGAATTTCA
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Submitted (18-UTL-2002) The Institute for Ge
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
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NEPSEKYNGYNGKYRERQHIINYLEDERIETISPOALIQNIYNDAYRAIFT
VAHNKLYKRELFSTLCZYPOGKLHEDEFLIYKLYKLKAKNIIFFRYNIYAYRIRENSIMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFLIFHWSDDFLSRVFGAFVPTITTGIVAFAŸIYYHSKSFYNPKYFRFIVTVSIPLIF
LICHQLLIGUDRIMLARLYSYKEVAYSFGYSLGATIQIVLNSINNAN PWFPDARK
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'note="identified by match to PFAM protein family HMM
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complement (3444. .4409)
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transI table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="cpsG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              producE="glycosyl transferase CpsN(V)"
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Pred. No. 2.5e-81;
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Best Local Similarity
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2206 8255	2263 8195			8075 2443	8046			7941	2623 7885							2920	2980	7526			7406	3156 7346		
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Mon May

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//organism="Streptcococcus agalactiae"
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Nucleic acids and proteins from streptococcus groups a & Patent: WO 0234771-A 12027 02-MAY-2002;
Chiron S.P.A. (IT); THE INSTITUTE FOR GENOMIC RESEARCH Location/Qualifiers
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Streptococcus agalactiae
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                            AAGAAAAGATACATAACAGATCTTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACTT
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/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/mol_e="texon:314"
/note="seq 1373 to long, original length:
2.160.266~replaced by~seq 1373: from 0.000.001 to
0.349.980~seq 1374: from 0.300.001 to 0.649.980~seq 1375:
from 0.600.001 to 0.949.980~seq 1376: from 0.900.001 to
1.249.980~seq 1377: from 1.200.001 to 1.549.980~seq 1378:
from 1.500.001 to 1.849.980~seq 1379: from 1.800.001 to
2.149.980~seq 1380: from 2.100.001 to 2.160.266"
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GAAAAAGTTGCAATAGTTAAGGAGTGCTTGTACTATTATGTTGACCGAGAAAATAGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCTGATTTAAATCG---TTCTGGAATTTTTATCATAATGATGGTTCATTATTTTGCAT
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Nucleic acids and proteins from straptococcus groups a b Patent: WO 03093306-A 1376 13-NOV-2003;

Chiron SRL (IT), THE INSTITUTE FOR GENOMIC RESEARCH (US)

Location/Qualifiers
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
                                                                                                           ACAACTTCTAGCATGACTGACCATCGCTTCCATTGCCTACTGGAATTTCA
                                                                                                                                                                                                                                                                                                                    linear
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Pred. No. 9.7e-82;
0; Mismatches 3382;
                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                  349980 bp DN Sequence 1376 from Patent WO03093306.
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Best Local Simi.
Matches 3323;
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6747
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	2384 AGAIAITAICAICI 273631 AGCITACAAAATAC 2444 AAITAITITAAATA 273602 ITITACTGTGTGGA 2504 AAAGAAAATAGGAI 273542 IGAICAITITE 2564 AAAACTAITITAATA
4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3 4 3	888888
133 INITIGANTCACATAACAATTCAAAAAATCTTGTTGCTTGCTTGTTTGGTAGTTTTTTGGAAGGG 27546 439 AAATGGTAACATTAACATTATACCTTTGATTTTTTGTTTTGTTTTTTTT	TANAGRACAGTGAAAGTTGTATTGTTGAGAGGAAGTAAAAGTAAAAGTATTGTTG
6 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4	3 4 8 5 8 5 8 5 .

ABARARAGTTTGGTGAACATGTAAATGATCATCAAGTAGAGTTTGTA 2146 sgaargardaarcercerrrragaaacraaragaagraarrrrarr 273752 rarrarrarceceaccarrireaarrrarrci------- 273498 AGAGAAGAGATTGTATATCATTGCTTCTTTCCAACAAACCGTAATGT 274472 274112 273992 CAATGTATAATTTTGATATCGTTGTAGATATTGAAAGGTTACAAAT 273812 graararraaaggagrigrgggargaaaarcaaraaaagcrcrtrarr 273692 -------ATGTTAGTTGCAA 273603 SAATAAAATTTTTATTAGATAGCCTTTATTTTGAAAGAAGAAAACTCG 273543 274352 2026 AAAAATACTTTCTTAGCTTTCAAAATTTTACGTGATGAAACCAGA 1606 TITAATCGATTGATAAAGGGATTGATTTATTGAAAAAAAATGGAAGT 1906 CAAATAGTTGAAAATTTAATGAGGATCAAGAAAATGAATAATAAAAA 2323 TITCICICAGGAGAAIGCACACCATIAGIICCTICAGAAIACCIGIAI 2443 PATTCTCAGGATTTATATGTTGAATTTACAAAAGATGAGCAAAAATAT 2503 VIATATGAACGAGTTAAATGTTACAGATTATTTCCTAATATATCAGAA 2563 ITCTGGTGCGGCCGTTGCTGTCCCTTTTTACATCGGAAAACTATT 1666 SATAATGGCTTATCATAATTTTTCTCAGATTTTTACTGGAGAGGGATAC 2383 NATGTACTGTTTAGAATTTTATTAAGAATGTATCGAGCTTTTGAATAC 2623 SATITIATATIGAAGTATITGAICGAGTIAAATAAATCIACAITAACITGG CCCGGTAACAGATATTTTATTGTTCAGTGGGAAGAAATGAAGAAGGT rcaaccercrrarraaagaagrrgaragarraaaagegacagerger **NTATITIATICAAACAGGATATICIGACTATATICCAGAATATIGCAAG** TCAGTTACAAAGAAATGGAACAATATAATTAACAAATCAGAAGTAGTT STITCTAAGCAAACTAACTITACATCAAATAATTATT---TITTTGT

272149 GITACAACTAATITTAITGATAAACAGAGGCCTTAAGAAT--AAGAATATTAITCAAAAGA 272092 271672 TAAAGTTAGTATTGTATATCTGTA---TAAACGTAATGGCGGTAAGCATTCAGCCTATAA 271616 271555 GTTÄTTAGAAGÄTGCAGTTGAAATTATTTTAAAGATTTTAGAGÄGCCTÄÄCGTTGTCTÄA 271496 272329 GAGCTTTTAAAAAGTTTAGATCCTTTGAGGATTCATGAGTGTTTTTCTAGCAAGGGAGATT 272270 271971 GITCITCATITATITCAGATICTCTAAAGATIAGAGTAAGGCTCATAAITGATITITIAT 271912 271911 TTGGATATGGTACTTATAGAATGCTTCTAAGGTTTAAAGTTAAAGAATAGTTATTAT 271852 271851 TGTAATAGAAAGGACGAAATGTTATATATTTTACTCCTACATTTAACAGAGGCTACGA 271792 271791 TTATCCTATC-TGTATGATTCTCTATGTAATCAGACAAATAAAATTTTATATGGTTGAT 271733 271495 TAGATATGTAGGCCT----TGTTTATCCTCGATATTCATTAAACCAAGGTAATAATTG 271442 3996 TIACTGATGTTTTTTTTTTTTTTTAAAAAAGTTTATGGAGTTAATGGGGGAAACA 4055 4475 4476 TATAGAAGTTGCAATGTTCGAGAATGCATGATAATATAACTGAGTATAATGCCGATAT 4535 4656 AGAAAATAATGTTTGGTGCAAGCTTTATTCACGAGATATTATAAAAGATATAAAATTCCA 4715 3876 TIAGAAAACAAIATITIATITIGGAIAIGGAAIAICCGAAIATICAGITIACGGGAACTIGG 3935 3936 CICGGAAGICATICAGGCTATATATATTTTTTTATAATCAGGAATAGTTGGGTTGATT 3995 4056 GCACTATTTTATTTTACATTAGCCATATTTTTCATATATGAAACAATAGATCCGATT 4115 TAATTITCATGTCTTAACGAGAGAAGAGCTGTAAAAGAATTITTGTCAGGATCTAATAT 4655 4716 AATTAATAATAGAAGTATTGGTGAGGATTTGCTTTTTAATTTTGGAGGTCTTGAACAAIGT 4775 272209 rcaaarargrerarargacaaaagigarrraacreereraaraagacargragag 272091 irgaigararararararccagaaarrarrraarccaaagaarraraacaggra 4356 GAAGAACGAIGGAAGAATTAAATTAACAAGAAAATTAATGGCGGTCTAGCAGATGCTCG TATGGAGATATATAGG-TGGAAAATTTGCTTGGATAAAAAAGCTAATAGTAATATTTGTA 3756 ATACTACTTATTATTTTAAATACTGAATTGCTTTACCATGAAATTTTGGCTGTTTATAAT 4116 ATTATTATTAGTACTATTCTTTTTTCTTCAATAGGTATTTGGAATAATATAAAA 4296 GGTTATTCTCGTAAATGATGGAAGTACTGATGATTCTGAGAAAATTTGCTTAAAACTATAT 4416 AAATTTCGGACTAGAACATGCAACAGGTAAATATATTGTTGCTTTTGTCGATTCTGATGACTA 271441 GTTGAATCCCAAAATATTAGAAGTTAATATTCCTGATTTAAAATATAAATATCACTTAAA 4176 AAGGATATGGAGACAAAAAATGAATGATTTAATTTTCAGTTATTGTACCAATTTATAATGT 4236 CCAAGATTATCTTGATAAATGTATTAACAGTATTATTAACCAAACATATACTAATTTAGA 3697 g

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CGTAACAGTTC 4835 CAAAAAAGGA 271264 ITGGAGAATTA 4895 III	5075 27103 27103 5135 27097 27091			AAGATTIACTT 5735
AACACGTGTAGTAGTTGATACTAGAGAATATTATTATAATTATGTCATTGGTAACAGTTC TTCGAAGGGGAATTTCTTATCAGAAGAAATAATTATTATATTTATCAAAAAGGGA GCTTATTAATCAGAAATTCTCTATAATAATATTTTGATTTAGTCACAAGATTGGGAAATTA GCTTATTAGAATTCTCTATAAATAATATTTGATTTAGACTACAAGATTAGAGAATTA ACTTTTGTCCCCAAAATAGGAAAATCTATTGTTTTGACTACAAGAGAGAA CCCCTTTAAGTTAAAAAAGAGAAAATTATGGGAAAAATTTTGAAGGGACTATTTCATTAGA GGTTAAATGTTTAAAATGTTATGGAGAAAAATTTTGAAGGGACTATTTTTTCATTAGA GGTTAAATGTTTAAAAATGTTATTCAAAGGATTGTTTGGATAATGATCCTAGTGCTAAGAAATCTTTTCCTAATATTTTGAACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGCT	ATTAGAGTCTTATCGAAAAGAATACGTAGATATCCATTTATTAAAGGGAAAGATATTTATAAAGGAATATTTTAAAGGGAAAAGATTTTTAAAGGGATAATTTTAAAGAGTATTTTAAAGAGTAATTACTTAAAAAAGGGTAATACCTACAAATGAAATGACTATTTAGTAACTAATAGTAACTAAAAAAATGAAATTTTGCCTAAACTAATATGTAATTTAGTAAAAAGAAGAGGTGGAAAATTTTGCCTAAACTAATATGTAATTTAAAAAAAA	CCAGTTATAATGTAGTAAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAAAT	270738 CAATCAGTTGCACGTAACACGGGGTACTTAGGTGTACGGGGAATTGCATTTTTAAACGAGGAATTGCATTTTTTTT	5676 AAGAAAGAITAATAACAGATCTITITCAAGAGAATCAITGGTIAGGAGAAGATTTACTT 5735 270443 GIPAITIATIGAGTAATCCAIAICCAGAAGGAAAATTCATGAAGAIATAGAIACATT 270384 5736 TITAATCTGCATTAITAAAGAATATAGATAGATAGTTATTTCACTGACATCTITAT 5795
4776 7 271323 7 4836 0 271263 7 271207 0 4956 0		5196 (270918 (5256 7 270858 7 5316 7 270798 7	270738 6 270678 6 270618 7 270618 7 5556 6 270558 7 5616 7	5676 A 270443 G 5736 B 270383 B 5796 B 270323 A 5886 B
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270264 GAGGCAATTCAAAATAATATTGTATTTATAAATCTAAATTTTCCACATAATACATCTTTA 270205 270144 GATITITAAATITATATGATACAGTIGATTATTACAGAAAAAAAATATAGAAAATATITTAAG 270085 270025 269915 AACGAGTGTATAGAAAGTGTTTTAGCTCAAACTTATTCAAATTTAGAAATTATTCTAGTT 269856 269855 AACGATGGCTCTACAGATAATTCCGGGGTATATTGTTATTATTAGAAAAAAGAGG 269796 269615 TGTTATGTTGAAAAAGAGAACAACATATTATAAATATCGTTTTAGAAGATGAAATGATA 269556 269438 TATCCAGTAGGGAAGTTACACGAAGATGAATTTTTAACCTATAAATTATATTTGAAAGCC 269379 269972 269971 AAGGA----ATGGATAAAGTTAGTATCATTATCCCAGTTTATAACGTTCAATCTTTCCTA 269916 269555 GAAACTATTAGTCCAGTACAAGCAATACAAAATATTTATAA---TTATGATGCCTATAGA 269499 6155 6275 6335 6395 5975 6396 AGTCGCCCCAAGGTGACTACTTAGCTTTTATAGACTCAGATGATTTTATTACATTCGGAG 6455 6456 TT---CATCCAACGTTTACACGAAGCAATTGAGAAGAAGAATGCCCTTGTGGCAGTTGCT 6512 6513 GGTTATG----ATAGGGTAGATGCTTCGGGGCATTTCTTAACAGCAGAGCCGCTTCCT 6566 6747 GAAAAAGTTGCAATAGTTAAGGAGTGCTTGTACTATTATGTTGACCGAGAAAATAGTATC 6806 269795 CGTATATTCGTTTTTCACAAAAATAATGGTGGTTTATCAGATGCTCGTAATTATGGAATT 5916 GACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTATAGCTTACTAATG 5976 TTTAAATACGGAAAACAGTCTATTTTGACAAATTTTTAATTTTTAGAAATCTTTATAAA 6036 AAATATTATTTTAACTTGTTAAAAGTATCTAACAAAATTCTTTGTCTAAAAATTTTTGT 270084 ACTATTCTCTTTAATAAGATTAGTGTGAAGGAAGGTTAAATATATTTATT 6096 ATAAGAATTGTTTCGAACAAAGTTTTTAAAAAATATTATGGTTATAATAGGAAGATATC 270024 TCCTCTATAAGATATTTCACTATTGTAAGAAAAATA-----TATAATTTGAGGTTATC ATGGATACTATTAGTAAAATTTCTATAATTGTACCTATATAATGTAGAAAAATATTA 6216 TCTAAATGTATAGATAGCATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTGGTG 6276 AATGACGGTAGTACGGATAATTCGGAAGAAATTTGTTTAGCATATGCGAAGAAGATAGT 6336 CGCATTCGTTATTTTAAAAAAGAGACGGCGGGCTATCAGATGCCCGTAATTATGGCATA 269675 GATGCAATCGAGAGAATGGTTGAATTTAGGGAGAAATATAATTCAGAAATTGTTTTAGGG 6567 ACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGT TITGAAAAGGGTAAGAITCAIGAAGAIGAATACTICACTIATGCTIGCTCTAIGAGTIA 269318 Argacitectracaratraaaagectacargereragaageacritaa 269269 6807 ACAACTTCTAGCATGACTGACCATCGCTTCCATTGCCTACTGGAATTTCA 6856 6156 6687

RESULT 12 AF355776 LOCUS DEFINITION

AP355776 17596 bp DNA linear BCT 29-APR-2001 Streptococcus agalactiae CNTC 1/82 type IV capsular polysaccharide synthesis operon, complete sequence.

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bdaiianaccefiltytqagrikknyvbkakeqmeqsgskflgiilnkvnesvatygdy
gdygnygkrdrkrk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLVPQI RKDGGPAI FSQNRVGRNGRI FRFYKFRSMRVDAEQI KKDLLVHNQMTGLMFK
LEDDPRI TKIGKFI RKTSI DELPQFYNVLKGDMSLVGTRPPTVDEYEKYNSTQKRRLS
FKPGITGLWQI SGRNNI TDFDBI VKLDVQY I NEWSI WSDI KI I LLITLKVVLLGTGAK"
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VEALSFDNIGEKRIQTFEGYSVITYSMKFYKYSHLIAKRFLDITGAIIGLLICGIVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |protein_id="AAK43606.1"
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LNSFLKYYRKYSYAKFSRDTKVVLJTNKDSLSKMTFRNKYDHNYIAVC1LDSSEKDCY
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product="beta-1, 4-galactosyltransferase enhancer CpsF"
protein_id="AAK43607.1"
db_xref="GI:13876775"
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                                                                                                                                                                                                                                                                                                                                   /producT="capsular polysaccharide chain length regulator/exporter CpsD" /protein_id="AAK43605.1"
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gene="cpsIVG"
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4595. .5944
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'gene="cpsF".
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QINSSHILKOKLFNDKHKRFKKRARYFLEENLVHFVASDMHNLDVRPPFLAEAVKIIC
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LASSQSVTKLNSITSQLQTSVQTNMTIDNINDLINNQLSTGQRFTVESQALTGHGSTG
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IPDGGGNQYDKLTHAGLYGVETSMKTLENLYDINLDYYARINFSSFLKLIDLLGGVTV
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'gene="type IV capsular polysaccharide synthesis operon"
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/product="putative capsular polysaccharide chain length
egulator CpsC"
                                                                                                                                                               1 (bases 1 to 17596)
McKinnon,K., Chaffin,D.O. and Rubens,C.E.
Direct Submission
Submitted (03-MAR-2001) Department of Infectious Disease,
Immunology and Rheumatcology, Children's Hospital and Regional
Medical Center, 4800 Sand Point Way NB, Seattle, WA 98105, USA
Location/Qualifiers
                                                                                             Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

    17596
        (organism="Streptococcus agalactiae" /mol_type="genomic DNA" /strain="CNTC 1/82" /db_xref="taxon:1311"

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db_xref="GI:13876770"
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/protein_id="AAK43604.1"
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/gene="cpsB"
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28. .933
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gene="cpsA"
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gene="cpsB"
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'gene="cpsC"
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TTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTAT 1323
                                                      TGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA
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                                                                                      TATTATATCTATTGAATTCATTTTTAAAATATTATCGAAAATATTCTTACGCTAAGTTTT
                                                                                                                                                                                             TATITIGAATCACATAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG
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ESYPACELPGEVNTGLGFGSI SRNPFIKENKI YEDTEYYSLKKTCYAI ITDLLTEGG
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Mismatches 3176;
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Streptococcus agalactiae strain NCDC SS615 capsular polysaccharide
biosynthesis gene cluster, partial sequence.
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Kong,F. and Gilbert,G.L.

Kong,F. and Gilbert,G.L.

Birect Submission

Submitted (02-JAN-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy

Rd., Sydney, NSW 2145, Australia

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           10313 CAACTTATAAATATTACTTATATTCAGATAAAATAGCCTTTGTACCAGAACCACTATATT
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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21635022
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TITLE
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JOURNAL
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KEYWORDS
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Similarity 59.2%; Pred. No. 2.6e-73; Conservative 0; Mismatches 916; Indels 41; Gaps 7; TGGCATTATTTGATAGATAGATAGCAGTTTCTGCAATCTTAACAAGTCATAACAA 75 TAGCGATTAAAACAGTTGAGTTTTTTTTGCAAGTTTGACATTAACATAATA 232 ATGCTGATTTAAAACAGTTATTTTTTTTTTTTTTATGATAGTTGATTATTTTGAT 132 OY ATGCTGATTTAAAAGCAATAAAGATTATTTTTTTTTTTT				649 552 709 612		
Best Local Similarity 59.2%; Pred. No. 2.6e-73; Matches 1390; Conservative 0; Mismatches 916; Indels 41; Gaps Qy 16 TGGCATTATTTGATAGATAGCAGTTGCAATTTCTGCAATCTTAACAGTATACCAA Db 173 TAGCGATGATTCAAACAGTTGTGTTTTTTTTTTGCAAGTTTAACATTAATTA	133 293 193 353	253 413 313 473	373 533 433	DD 593 GGAAIAAATACGACCATAATTATATGTCTGTCTGCAFCTTGGACTCCTCTGAAAAGG Qy 493 AAATAGATAAATTAATCATTACGCTCTATTATTCTGGGAAGAAGCTATAGGGT Qy 650 ATTGTTATGAACATAACTGCTTAAGGATAATAACAAAAGAGGTCTTACTTCAG Qy 553 TTTCACAAGAGGAAGTGGTCGACCACTTATAAATCTACCAAGTGGTTTTTAGACG Db 710 AGTTAACCTGCTTAACTGTTATAACTATAACATACCATTGAATTATTTGGTA	613 770 664 830 724 890	784 950 844 1010 904 1070 1130

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VEKHNSKLIINKDALTSELTCLTVDOAFINIFIELFGKYOLDIINDIEAMGYTVNVN
PALSFDNIGERRIOTERGYSVITYSWKFYKKYSHLIAKRFLDITGALIGLIGGIVAL
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                                                                2324 AAAGAGTTATTCTTGAAATATGAATTAGATTATATTTTGAATATCAGTGAATTAGAGAAT 2383
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                                                                                                                                                                                                                                                    BCT 07-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                       4513 bp DNA linear BCT 07-JAN-20
Streptococcus agalactiae strain SG99/077 capsular polysaccharide
biosynthesis gene cluster, partial sequence.
AF363060
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Kong, F. and Gilbert, G.L.

Kong, F. and Gilbert, G.L.

Birect Submission

Submitted (22-MAR-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy

Road, Sydney, NSW 2145, Australia

Location/Qualifiers
                     AGAAGAATTTTACAAGATAATAATATTTTATTATAGAAAATATAGATGATTTGTTTGAA
                                                                                                                AAAATTATTGAAGTTTCTAAGCAAAC---TAACTTTACATCAAATAATTTTTTTTTGT
                                                                                                                                                         2384 ATTATTAAGGAAAAAATATATCTACTAGTAAAGTAATATCACAAAACAATGATTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L. Serotype identification of group B streptococci by PCR and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus agalactiae
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,

    4513
    organism="Streptococcus agalactiae"

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දි දි	193 AAACATTTAACTATAGTATTAATATTTTGTAATTTTTCTTACGGGAGTATCATTTTGTTGG 252 153 TGGTATTGAAATACAGCTTTTACCATATTTTCATAAGTTCATTATTTTTTTA 112	qq	
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රු පු	313 TGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372 	Ωρ	GAAT
ठे व	TCTATCAAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT	ጵ	1427 GITAAAACGITTIGGAAGGAAGAAGAAGGACGITIT
8 &	553 CACGAGATACCAAAGITTIGATAAGGAATAAGGATICTITATCAAAAATGACCTITA 592 433 TATITGAATGACAAAATICAAAAAAATCTGTGTGGTAGTITTTAGGTAGGA 492	ò	
ορ	593 GGAATAAATACGACCATAATTATTGCTGTCTGCATCTTGGACTCCTCTGAAAAGG 649	음 &	1664 TAGGAGTATTCTAAGAGAAGAGATTGTATATCAT 1547 CATTAATTTAGTGAAAAATACTTTCTTAGCTTTTC
& 8	493 AAATAGATAAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT 552 	2 음	1724 CAAAACTIGGIAAAAAIACIAITCIAGCITII
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음 ;	AGTTAACCTGCTTAACTGTTGATCAAGCTTTTATTAACATACCCATTGAATTATTGGTA	č	
ž 8	613 TAAASCANITCGTITCAGATTITAAGTIGTTAGGTATTGANGTAAGGGTTG 663 770 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGAAGTGATGTGTTA 829	Dp	1844 TGGTTGTAAGACCGTTTATATAGAGGTTTTCGAC
ð		දු ද	1727 AAAACTAGTTTATCCCGTAACAGATATTTTTATT
Ωp	830 AIGTAGAGCACTTAGCTTTGATAATAGGAGAAAGCGAATCCAAACTTTTGAAGGAT 889	3 8	170* AMALINGIGIALCUSTRACAGALAMILIALI 1787 ATATCCTAAATCTATAACTTGGGGAGTATTTT
<i>አ</i> ብ	724 ATRGCATIGTAACTITITCCACAAATTITTATAAGCCTAGTCATATCATGATGAAGGGC 783 890 ATAGTGTTATTACATATAATTCTAGAAATTGTAAAATATAGTCACCTATATAAAAAGGAT 949	qq	
È	TTTTGGATATACTCGGAGCGGTAGTCGGGTTAATTTGTGGTATAGTTTCTATTTTGT	<i>≿</i> 8	1847 CATGAACAACAGTTTAATCGATTGATAAAAGAGA
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Š	AGAATGGACGCATATTTACATTCTACAAGTTTCGATGATGTATGT	8	
qq	1070 GTAATGGTAGGATTTTTAGATTCTATAAATTCAGATCAATGCGAGTAGATGCAGAACAAA 1129	<u>8</u> 8	2144 IGGTCAAAATITCICICATATGATGATGAACT 2027 ATTTGCCACGGAGGCCCGCTACTTTTATGAATT
& 8	964 GCAAAAAAGACTTGCTCAGCCAAAACCAGATGCAAGGGGGGGTATGTTTTAAAAAAGATTTATTAGTAAGAATGATCAAATCAAATCAAATGAAGGGGGGGG	7 A	
۸۵ .	AAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGT	& A	2087 TTGTTTCCTAGACAAAAAGTATGGTGAACATC
යි යි	1185 CGATGATCCTAGAATTACTAAAATAGGAAAATTTATTCG-AAAAACAAGCATAGATGAGT 1243 1084 TACCACAGTTTTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTA 1143	à	2147 AGAAGAATTTTACAAGATAATAATATTTTATTTZ
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λ G	1144 CAGTIGATGAATITGAAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAG 1203 	දු දු	220/ MAMATTATTGANGTTTCTANGCAAACTANCT 2384 ATTATTANGGAAAAAAATATCTACTAGTAAAA
ò		č d	2264 GAAAGATTAAAACAAATAGTTGAAAAATTTAATG
_{අය} .	1364 GAATCACTGGTTTGTGGCAAATATCTGGTAGAAATATATAT		

CATGITACTITCCAACAAATCGCAATCT 1546 TCCCCTTCTTTACATCGGAAAACTATT 1666 TTGTTCAGTGGGAAGAATGAAGAAGGT 1786 TTTAATGATTTTTGTAACAGTAGGAACT 1846 TTCATTATCCAAAGGAAAAAACAATTA 2086 CTTTACATCAAATAATATTTTTTTTT 2263 CAGGGGACATTTGACTCACTTGTATTT 1426 || |||| | || || || CTCAGATTGTCAG 2143 TATAGAAATATAGATGATTTGTTTGAA 2206 ||| |TATTTTGAATATCAGTGAATTAGAGAAT 2383 FGAGGATCAAGAAATGAATAAAAA 2323 ACTAICTGGICAGAIATTAAAAITTIAT 1323 GTGGTGGTCATCTAGCACACTTGAACCT 1603 TTTGGGTAACATTTGATAAAGAGGATGC 1486 ICAAAATTTTACGTGATGAGAAACCAGA 1606 ATCGAGTTAATAAATCTACATTAACTGG 1726 ITCTGACTATATTCCAGAATATTGCAAG 1966 ACAATATATAACAAATCAGAAGTAGTT 2026 CTCTTACATGAAAGAAGCTGAGATTGTT 2203 IGTAAATGATCATCAAGTAGAGTTTGTA 2146 SCAAGTAAGTAAAAGTA-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHSLFKNPDFDRILAAFNSLIIGIVSLAFYHYYKNTTLELDKILKAFLFNGLILFFLG
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YMKLRNYSIMTIGVVLLFTFILDIGSGSRAGIVAILAQMFILLLNTVVVKKKTIKFLL
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Best Local Similarity 59.2
Matches 1390; Conservative
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Kong, F. and Gilbert, G.L.

Direct Submission

Submitted (02-7AN-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Rd., Sydney, NSW 2145, Australia

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 4522)
Kong,F., Gowan,S., Martin,D., James,G. and Gilbert,G.L.
Serotype identification of group B streptococci by PCR and
                                                                                                                                                                                                                                                                                               Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Streptococcus agalactiae strain NCDC SS700 cs
biosynthesis gene cluster, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Microbiol. 40 (1), 216-226 (2002)
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482 TATTGTATCTATTGAATTCATTTTTAAAATATTATCGAAAATATTCTTACGCTAAGTTTT 541	
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1493 TCCTAACACTAAAGTACTTACTTGGGACAGGTGCTAAGTAAAGGTAAGGTTTGAAAG 1552	AF332893 4888 bp LOCUS AF332893 1989 DEFINITION STrentococcus acalactiae strain 09
1373TATGAAAGTTTGTTTGGTCGGTTCTTCAGGGGGACATTTGACTCACTGTTTT 1426	ACCESSION AF332893
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DNA linear BCT 07-JAN-2002 090 capsular polysaccharide 11 sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 IGGIÁTTGAAATÁCAGCTÍTTACTATATTTTCATATCAAGTTCATTÁTTTTTTTTTTT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ATGCTGATTTAAATCG---TTCTGGAATTTTTATCATAATGATGGTTCATTATTTTGCAT
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Kong,F. and Gilbert,G.L.

Birect Submission

Submitted (02-JAM-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Rd., Sydney, NSW 2145, Australia

Location/Qualifiers
                                                                                                                                  Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L.
Serotype identification of group B streptococci by PCR and
                Streptococcus agalactiae
Streptococcus agalactiae
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;

    4888
/organism="Streptococcus agalactiae"
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/strain="090"

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Gaps

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59.2%; Pred. No. 2.6e-73;
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Best Local Similarity 59.2
Matches 1390; Conservative
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Kong,F. and Gilbert,G.L.
Direct Submission
Submitted (22-MAR-2001) CIDMLS, ICPMR, Westmead Hospital, Darcy
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
                                                                                     Streptococcus.
Loasea 1 to 4888)
Kong,F., Gowan,S., Martin,D., James,G. and Gilbert,G.L.
Serotype identification of group B streptococci by PCR and
                                            Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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J. Clin. Microbiol. 40 (1), 216-226 (2002)
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Matches 1389; Conservative (
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                                                                                           Streptococcus.
I bases I to 4888)
Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L.
Serotype identification of group B streptococci by PCR and
                   Streptococcus agalactiae
Streptococcus agalactiae
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J. Clin. Microbiol. 40 (1), 216-226 (2002)
21635022
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2 (bases 1 to 4888)
2 (bases 1 to 4888)
Kong.F. and Gilbert,G.L.
Direct Submission
Submitted (22-MAR-2001) CIDMLS, ICPM
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
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KEYWORDS
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75

Gaps

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1726. 4700

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AAACATTTAACTATAGTATAATATTTGCAATTTTTTTTTGCTGGGAGTATCATTTTTGTTGG
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                                                                                                                                                                                                                                                                                                                                                     ICPMR, Westmead Hospital, Darcy
                                                                                           Streptococcus.
I bases 1 to 4888)
Kong.F., Gowan,S., Martin,D., James,G. and Gilbert,G.L.
Serotype identification of group B streptococci by PCR and
                     Streptococcus agalactiae
Streptococcus agalactiae
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;

    .4888
/organism="Streptococcus agalactiae"
/mol type="genomic DNA"
/strain="SG99/276"

                                                                                                                                                                    sequencing
J. Clin. Microbiol. 40 (1), 216-226 (2002)
21635022
                                                                                                                                                                                                                                                                            2 (bases 1 to 4888)

Kong, F. and Gilbert, G.L.

Direct Submission

Submitted (22-MAR-2011) CIDMLS, IC

Road, Sydney, NSW 2145, Australia

Location/Qualifiers
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1427 GTTAAAACGTTTTGGAAGGAAGAACGTTTTTGGGTAACATTTGATAAAGAGGATGC 1486	1607 TGTTATTATTTCATCTGGTGCGGCCGTTGCTGCCCTTCTTTTACATCGGAAAACTATT 1666 1793 TGTTATCATCTGGTGCCGCTGTAGCAGTACCATTCTTTTATATTGGTAAGTTATT 1852 1667 TGGAGCAAAGACGATTTATATTGAAGTATTTGATCGAGTTAATATGGTAAGTTATT 1852 1667 TGGAGCAAAGAGGATTTATATTGATCGAGGATAATAAAATTTGATCGACAGATAAAACCAACTTTGACGG 1726	1787 ATATCCTAAATCTTAACCTTGGGGGGTATTTTTAATGATTTTTGTAACGGTAGGAACT 1846 1973 TTATCCTAAGGCAATTAACTTTGGGGGAATTTTTTTTTT	2153 TGGTCAAAATTTCTCTCATATGATATGAACTCTTACATGAAGAAGAAGAATTTCTTCTCTACATAGAACTCTGAATTGTT 2212 2027 ATTTGCCACGGAGGCCCCCTACTTTATGAATTCATTATCCAAAGGAAAAAACATTA 2086 2213 ATCACACATGGCGGCCCCACCTTTATGAATGCAGTTTCTAAAGGAAAAAAACATT 2272 2087 TTGTTTCCTAGACAAAAAAGTTATGGTGAAAAATGATCATCAAGTAGAGTTTGTA 2146 2273 GTGGTTCCTAGACAAAAAAATTTGGAGAGATATATTATTTTG 2332 2147 AGAAGAATTTACAAGAAAATATTTTATTATAGAAAATATAGATGATTTTTTG 2332 2147 AGAAGAATTTACAAAATAATATTTATTTATAGAAAATATAGATTTGTTTG	OY 2207 AAAATTATTGAAGTTTCTAAGCAAACTAACTTTACTCTAAATAATATTTTTTTTTT
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AGTTAACCTGCTTAACTGTTGATCAAGCTTTTATTAACATACCCATTGAATTATTTGGTA 1034
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Luclassified.

(bases 1 to 6865)

AUTHORS

Miyake, K., Watanabe, M. and Iijima, S.

TITLE

Beta-1,3-galactosyltransferase and DNA encoding the enzyme

FROWHENT

COMMENT

OS Streptococcus agalactiae Type ID

PN JP 2002199885-A/2

PD 16-JUL-2002

PP 05-JAN-2001

PP 05-JAN-2001

PP 05-JAN-2001

PP (C12N9/10,C12R1:19),(C12P19/28//(C12N15/00,C12N15/00,PC)

C12N15/09,C12N1/21,C12N9/10,C12P19/28//(C12N15/00,C12N15/00,PC)

C12N15/09,C12N1:19),(C12P19/28,C12R1:19),C12N15/00,PC

C12N15/09,C12N1:19),(C12P19/28,C12R1:19),C12N15/00,PC

C12N15/09,C12N1:19),(C12P19/28,C12R1:19),C12N15/00,PC

C12N15/09,C12N1:46)

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                                               .035 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 1094
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TAAAGCAATTC------GTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTG
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1813. 1813.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (E-mail:miyake@proc.nubio.nagoya-u.ac.jp, Tel:81-52-789-4278,
Fax:81-52-789-3221)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="beta-1,4-galactosyltransferase"
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/mol type="genomic DNA"
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/function="putative CP polymerase"
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                                                                                                                                                 442. .1791
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442. .1791
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1815. .2264
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'evidence=not ε
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/gene="cpsibG"
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2842. .3981
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                                                                                                                                                                          1787 ATATCCTAAATCTATTAACTTGGGGAGTATTTTTAATGATTTTTGTAACAGTAGGAACT 1846
                                                                                                                                                                                                2229 TTATCCTAAGGCAATTAATTTAGGAGGAATTTTTTAATGATTTTTGTCACAGGGGGGACA 2288
                                                                                                                                                                                                                                                   1907 ATAACCGACGAAATATTTATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAG 1966
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Miyake,K., Watanabe,M. and Iijima,S.
Direct Submission
Submitted (01-NOV-2000) Katsuhide Miyake, Nagoya University, Grad.
Sch. of Engineering, Dept. of Biotechnology; Chikusa-ku, Furo-cho, Nagoya, Alchi 464-8603, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae cpslbb, cpslbF, cpslbG, cpslbH, cpslbI, cpslbK, cpslbE, cpslbL, ab050723
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HLICHOLLNOLDRIMLARLYSTKEVAMYSFCYSLGMIIQIVLNSINMAMIPWSIPLIF
EKLLOLSTYISRYLYGUFLTLGYLLYPPELLAQIMGGDQYSSSVQFISLIIVSFPLVF
LYTFPVNIOPFYAMYTWNPIGTLLAAGVWALLANIL PHYAAYGAAATIISVSTALLI
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/protein_id="BAB21605.1"
/db_xref="G1:12697602"
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/gene="cpsibL"
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/gene="neuB"
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YIKQRYSSGMMILGALLSTIILPIGSGSRAGIIVVLLQVIILLATIVIKRQTIRFFL
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KQYIYSAILQDFYKEKSYIDITKITNYFQEYVIKKRYTQQELSKYFELKSTPSITIRK
                                                                                                                                                                                                                                      function="beta-1,3-N-acetylglucosaminyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="beta-1,3-galactosyltransferase"
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TAATAAATCTACATTAACTGG 1726 AGTGGGAAGAATGAAGAAGGT 1786 BATTITIGIAACAGTAGGAACT 1846 rttattgaaaaaaaggaagt 1906 CTATATTCCAGAATATTGCAAG 1966 ATCCAAAGGAAAAAAACAATTA 2086 AATATAGATGATTTGTTTGAA 2206 |||||| BAATATCAGTGAATTAGAGAAT 2647 ATCAAATAATTTTTTTTG 2263 linear BCT 07-JAN-2002 sular polysaccharide nce. PATTAACAAATCAGAAGTAGTT 2026 nd Gilbert, G.L. reptococcaceae;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 IGGIATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493 AAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGCGATGATTCAAACAGTTGTAGTTTATTTTTCTGCAAGTTTGACATTAACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 CTCCCAATTTTAAAAGCAATAAAGATTTATTGTTTGTTCTATTGATACATTATATTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 TATTTGAATCACATAAACAAATTCAAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCTGATTTAAATCG---TTCTGGAATTTTTTATCATAATGATGGTTCATTATTTTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 TTTATCTTTCTGATTTTTACAGAGACTTTTGGAGTCGTGGCTATCTTGAAGAGTTTTAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 TCTATCAAAAAAAAGACGATTCTAATTACAACGCTGAACGATGGGAAAATATGCAAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 726.8; DB 1;
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Best Local Similarity 59.2
Matches 1366; Conservative
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DLKKHNSLRIINKDALFTSELTCLTYDQAFINIFIELFGRYQIQDIINDIEAMGYIVNVN
VEALSFDNIGEKRIQTFEGSTSVITYSMKFYKYSHLIAKRFLDITGAIIGLLICGIVAI
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QNCQWSKFLSYDDMNSYMKBAEIVITHGGPATFWSVISLGKLPVVVPRRKQFGEHIND
HQIQFLKKIAHLYPLAWIEDVDGLAEALKRNIATEKYQGNNDMFCHKLEKIIGEI"
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| db_xref="d1:1803338"
| translation="WRYYLDLDYSLFYALWVLILVPNOWYOFLIITIIVLLLWKSEF
RISISNSSILFILWLFIILFAILIRGTQEDITFQRFIAELLKLISTGYALFFYNYYRK
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LEDDPRITKIGKFIRKTSIDELPQFYNVLKGDMSLVGTRPPTVDEYEKYNSTQKRRLS
FKPGITGLWQISGRNNITDPDEIVKLDVQYINEWSIWSDIKIILLTLKVVLLGTGAK"
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YYEVFDRIDKPTLTGKLVYPVTDKFIVQWEEMKKVYPKAINLGGIF"
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'translation="AKEQMEQSGSKFLGIILNKVNESVATYGDYGNYGKRDRKRK"
                                                   Darcy
                                                 ICPMR, Westmead Hospital,
                                                                                                                          /organism="Streptococcus agalactiae"
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/strain="M781"
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db_xref="GI:18033336"
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Kong, F. and Gilbert, G.L.
Direct Submission
Submitted (02-JAN-2001) CIDMLS, I
Rd., Sydney, NSW 2145, Australia
Location/Qualifiers
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/transl_table=11
/product="CpsE"
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132

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192 352 412 312 472

532 432 592 492

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4768 bp DNA linear BCT 07-JAN-2002
Streptococcus agalactiae strain SG99/143 capsular polysaccharide
biosynthesis gene cluster, partial sequence.
AF533055
AF363055.1 GI:18029139
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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1 (has 1 to 4768)
Kong. F., Gowan, S., Martin, D., James, G. and Gilbert, G.L. Serotype identification of group B streptococci by PCR
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Kong, F. and Gilbert, G.L.

Direct Submission
Submitted (22-MAR-2001) CIDMLS, IC
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
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Pred. No. 5.1e-73;
0; Mismatches 902; Indels 38;
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FLYDIKKDGGPALFSQNYGRNER IFFFYKFRSMVDAEQIKKDLJVHNQMTGLMFK
LEDDPR ITKLGKFIRKTSIDELPGYNVLKGDMSLVGTRPPTVDEYEKYNSTQKRRLS
FKPGITGLWQISGRNNITDFDEI VKLDVQYINEWSIMSDIKIILLTLKVVLLGTGAK"
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HQIQFLKKIAHLYPLAWIEDVDGLABALKRNIATEKYQGNNDMFCHKLEKIIGEI"
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ADFNSSVVRNVVKVNYFVLFLITVLYLFFPMLKPTLFGRELFSIEWFPHMRIRLAAYF
EYATLIGQFILFSYPILFLKPQKHMENILISLLLTICSYFSGARILLVCMLVLLASLL
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ESIIEVLKGNILFGQGIRIPSSEGIFLGSHSTYISVFYRTSLLGIVLYFSAFILLYKE
AISKNYKIYRLFFYTLLCYTLFEEIDPNHWSIVLLFSTFGIVGRAKK"
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AF363056 4768 bp DNA linear BCT 07-JAN-2002 Streptococcus agalactiae strain GB00/031 capsular polysaccharide biosynthesis gene cluster, partial sequence.
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Streptococcus agalactiae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
1 (bases 1 to 4768)
Kong, F., Gowan, S., Martin, D., James, G. and Gilbert, G.L.
Serotype identification of group B streptococci by PCR an
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2 (Dases 1 to 4768)
2 Nong, F. and Gilbert, G.L.
Direct Submission
Submitted (22-MRA-2001) CIDMLS, ICPMR, Westmead
Road, Sydney, NSW 2145, Australia
Location/Qualifiers
1. 4768
Applementation Contains Streptococcus agalactiae"
(mol type="genomic DNA"
/strain="GBOO/031"
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ATAGTGTTATTACATATTCTATATATTATATATATATCTCACCTTATAGCAAAACGAT 949
                                                                                                                                                                                                                  TITIGGATATACTCGGAGCGGTAGTCGGGTTAATTTGTGGGTATAGFTTCTATTTGT 843
                                                          ATATTAATTCATTCGGTTTTACTGCGTTGAAAAACAAAAAATCCAACTGCTAGGTGACC 723
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NSGEI CDNLSQEDNR I LVFHKKNGGVSSARNLGLDKSTGEF I TFVDSDDFVAPNMI ET
MLKNL I TENAD I AEVDFDI SNERDYRKKRRNFYKVFKNNNSLKEFLSGNRVENI VCT
                                                                                                                                                   KLYKKSIIGNLRFDENLKIGEDLLFNCKLLCQEHRIVVDTTSSLYTYRIVKTSVMNQK
FNENSLDFITIFNEISSLVPARLANYVEAKFLREKIKCLRKMFELGSNIDNKIKVQRE
IFFKDIKSYPFYKAVKYLSLKGLLSFYLMKCSPKLYVMAYRRFQKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MIKKIEKDLISVIVPIYNVEDYLVECIESLIVQTYRNIEILLIN
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                                                                                       translation="MKEKVTVIIPIYNSEAYLKECVQSVLQQTHPLIEVILIDDGSTD"
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/db_xref="GI:18029154"
                       /product="Cps1"
/protein_id="AAL56372.1"
/db_xref="G1:18029153"
  transl table=11
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trans[ table=11
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/gene="cpsJ"
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DLKHNSLR IINKDALTSELTCLTVDQAFINIPIELFGKYQIQDIINDIBAMGVIVNVN
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FLVPQIRKDGGPAIFSVNGRNGRIFFFFFFRRSMRVDAEQIKKDLJVHNQMTGLMFF
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FKPGITGLMQISGRNNITDFDBIVKLDVQYINEWSIWSDIKIILLTLKVVLLGTGRKF
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HQIQFLKKIAHLYPLAWIEDVDGLAEALKRNIATEKYQGNNDMFCHKLEKIIGEI"
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DYLIFKTHMALTKKAPFILGMTFLFTACFSYNUSIIEKIIMYRNGSTITRNIVYQ
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178. .1527
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                                                                                     gene="cpsD"
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gene="cpsG"
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gene="cpsG"
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gene="cpsH"
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NYPSQLLQKITVSILKDTRVISISVEDANPKMSQKLANSVREAAVSKIKAVTQVEDI
TTLEKKNLPRAPSSPNIKKNVLIGFIVGAGLSTIVLVIMGILDDRVNTEEDIEKVLGI
TSLGIVPDLNKL"
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DAAIIANAGOGFILVTQAGRIKRNYVEKAKAKEQMEQSGSKFLGIILNKVNESVATYGDY
GNYGKRDRKRK"
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LINSFLKYYRAFRSPATRYLYLYNDSLSKATFRNKYDHYTAVCTLDSSENDCY
DLAKTNSLR I INKDALFTSELTCLTVDQAFIN IP IELFGKYQLQD I INDI EAMGYLYNVN
VEALSFDNIGEKRIQFPRGYSVITYSMKFYKYSHLIAKRFLDITGAIIGLICGIVAI
FLYDIRKDGGPAIFSQNYKORNGRI FRFYKKRSWUDAGDIKKDLLYNNGWTGLMFK
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FKPGITGLMQISGRNNITDFDBIVKLDVQYINEWSIWSDIKIILLTLKVVLLGTGAK
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note="glucosyl transferase; previously described as CpsD"
citation=[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="putative polysaccharide chain length regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="autophosphorylating tryosine kinase"
note="CPS chain length regulator/exporter"
                                                                                                                                             function="tyrosine phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein id="AAB00362.1".
                                                                                                                                                                                                                                                                            protein_id="AAB00361.1"
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trans1_table=11
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trans[ table=)
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3316. .3321
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4755. .4761
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4770. .6119
                                          gene="cpsB"
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1029. .4718
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.2576
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RHDKANLSKMGQRFIDYLLEEVSFNHKNKQS"
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                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (16.MAY-1996) Division of Infectious Disease, Immunology
and Rheumatology, Children's Hospital and Regional Medical Center,
4800 Sand Point Way N.E., Seattle, WA 98105, USA
6 (bases 1 to 17276)
Chaffin,D.O., Yim,H.H., Beres,S.B., Sweet,E.S., Nittayajarn,A. and
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TNNLNKTASYSEIEMSVVVPKOSKITNIEAVSKLAAPVKNDTSNITDLIEHIKSEKGI
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Submitted (29-JUN-1999) Division of Infectious Disease, Immunology
and Rheumatology, Children's Hospital and Regional Medical Center,
4800 Sand Point Way N.E., Seattle, WA 98105, USA
On Sep 5, 1999 this sequence version replaced gi:1323729.
Location/Qualifiers
                                                                                                                                      Submitted (27-JAN-1993) Division of Infectious Disease, Immunology and Rheumatology, Children's Hospital and Regional Medical Center, 4800 Sand Point Way N.E., Seattle, WA 98105, USA 5 (Dases 4495 to 6194)
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EIVYHCFFPTNRNVKNLVKONTILAFKVLRKERPDVIISSGAAVAVPFFYIGKLFGCKT
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                                                                                                                                                                                                                                                                                                                              New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination.
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                   termination codon
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P-PSDB; AAY68970, AAY68971, AAY68972, AAY68973, AAY68974, AAY68975.
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an unspecified
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2. .721
// note= "ORF 22; encodes AAY68950"
complement(822. .2079)
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note= "ORF 2Y; encodes AAY68951"
:202. .2936
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note= "Cps2F; encodes AAY68958"
1262. .10419
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note= "Cps2C; encodes AAY68955"
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089. .9258
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18401. .18904
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'note= "Cps2A; encodes AAY68953"
504. .5193
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note= "Cps2B; encodes AAY68954
         6961 ATCATTGGTTGAGCAAACAGCAAAAGAAGCTT 6992
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/transl_except= (pos: 1.
/note= "Cps2H; Xaa is a
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"Cps2D; encodes
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/note= "Cps2J;
14574. .15578
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3583. .14581
                                                                                                                       standard; DNA; 26281
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The present sequence represents the capsular gene cluster of Streptococcus suis serotype 2. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins are involved in regulation (CpsA), chain length determination (CpsB, CpsC), export (CpsC), and biosynthesis (CpsE, CpsF, CpsG, CpsH, CpsK). The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for reducing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in humans or animals, e.g. against S. suis in pigs
                                                                                                                                              amino acid; encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wew nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination.
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P-PSDBB; AAYG8950, AAYG8951, AAYG8952, AAYG8953, AAYG8954, AAYG8955,
AAYG8956, AAXG8951, AAYG8958, AAYG8959, AAYG8960, AAYG8961, AAYG8962,
AAYG8963, AAYG8964, AAYG8965, AAYG8966, AAYG8967, AAYG8969, AAYG8969
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Thr)
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Pro)
Xaa)
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Ser)
          (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE
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"Cps2P; encodes AAY68965"
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22-JUL-1998;
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Gaps

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Indels

17.1%; Score 1195.8; DB 3; 78.9%; Pred. No. 1.1e-151; ive 0; Mismatches 382;

Best Local Similarity 78.9 Matches 1437; Conservative

Query Match

DB 3; Length 26281;

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14481 CGICCICIGITITIAAAAGAATIATGTAATTAATIGTIGCTAAIAATITGTITAAAATIT 14540
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The present sequence is an eps operon from Streptococcus thermophilus. Proteins ancoded by the eps operon function in expolygaccharide (BPS) synthesis. The operon is useful for producing chimeric eps operons, for optimising production of BPS in lactic acid bacteria. EPS impart texture, mouth feel and theological properties to fermented food products (e.g. yoghurt). They function as thickeners, to provide free-flowing and texture, and may also have biological activities beneficial to health
                                                                                                                                                       nucleic acid fragments containing exopolysaccharide operon, useful for increasing exopolysacchride synthesis in lactic acid bacteria
                                                                                                ပဲ
                                      (INRG ) INRA INST NAT RECH ACRONOMIQUE.
(DANO-) CIE DANONE SA GERVAIS.
(RHOD ) RHODIA CHIM.
                                                                                                Fremaux
                                                                                                                                                                                               Claim 9; Page 75-80; 144pp; French
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.8%;
Matches 1484; Conservative (
                                                                                                Besancon-Yoshpe I,
              18-APR-2000; 2000FR-00004972
                                                                                                                           WPI; 2002-017616/02.
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                                                                                                            Gaps
Sequence 17468 BP; 5871 A; 2455 C; 3307 G; 5835 T; 0 U; 0 Other;
                                                                                                         41;
                                                       Length 17468;
                                                                                                         Indels
                                                    Score 955.6; DB 6;
Pred. No. 1.9e-119;
0; Mismatches 729;
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TCTACATTAACTGGAAAACTAGTTTATCCCGTAACAGATATTTTTATTGTTCAGTGGGAA
                                                                                                                      GCAAAAAGCCAATTGTTGTGCCTAGACAAGAAAAGTTTGGTGAACATGTCAATGACCATC
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The invention relates to a novel strain of a lactic acid bacterium that contains at least one of 8 specific nucleic acid sequences all of which are defined in the specification. The bacterium of the invention may be useful during food preparation particularly that of beverages and meat, cereal, or dairy products e.g. fermented milk, yoghurt, 'matured' cream, dessert cream, cheese, soft cheese, cheese spreads, cottage cheese, milk-based drinks, dairy product retentates and baby milk, where the products are derived from an animal and/or plant. The current sequence is that of the Streptococcus thermophilus CNCM 1-2980 polysaccharide synthesis-related operon DNA of the invention.
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                                                                                                                                                                                                                                                                                                                                  New strain of lactic acid bacteria, useful for preparation of foods and pharmaceuticals, especially fermented dairy products, contains genes involved in polysaccharide biosynthesis.
                /product= "Transposase IS1193 protein"
/note= "The corresponding protein sequence is not shown
shown within the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617 GCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGCGTTGATATTAATTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16032 BP; 5191 A; 2323 C; 3188 G; 5330 T; 0 U; 0 Other;
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Pred. No. 1.6e-110;
); Mismatches 655;
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                                                                                                                                                                                                                                                               Huppert S, Fremaux
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66.8%;
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                                                                                     FR2852604-A1
                                                                                                                         24-SEP-2004
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/note= "The corresponding protein sequence is not shown
shown within the specification. The CDS has a prokaryotic
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he CDS has a prokaryotic
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note= "The corresponding protein sequence is not shown
hown within the specification"
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'note= "The corresponding protein sequence is not shown
shown within the specification"
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fnote = "The corresponding protein sequence is not shown
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 'product= "Polysaccharide polymerisation/export-related
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'product= "Undecaprenyl-phosphate glycosyltransferase
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shown within the specification"
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shown within the specification"
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shown within the specification. No start codon."
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/note= "The corresponding protein se
shown within the specification. The
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133 HITTININICCOCHAIGCAGATGAATITGGATATAGAGGATATATAGAGGATATAGAGGATATAGAGGATATAGAGGATATAGAGGATATAGAGGATAGAGAGGATAGAGGATAGAGGATAGAGGATAGAGAGGATAGAGGATAGAGGATAGAGGATAGAGGATAGAGAGAGGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

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1339 TAGITITIATIAGGITAINTENDATARIAGGIAAAATGGGAAAGATAITICTITITI 1456 43209 GIANCGAACCTIANAAAAAGAATTITICTIATAAAGAGGAAACAAACAAACAAACAAACAAAAAAAAAA	GGTTATTCTCGTAAATGATGAGAGTACTGATGATGAGGAAATTTGCTTAAACTATAT TTATCCTATC
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4321 GANGARITTINAGGIANITITIAAGAGITTICGARGAANTCATTINCTGAGAGGGATAC 2383 4221 TANINITGCANITITIAAGATATTITICAGAATTITICAGATTINCTGAGATTICAGAATTACTGAGAAATTA 2411 4171 AGCTIACAANITGATATATTITIATAAATTITITIAAAAAACCTITAATTICAGAATTACTGAAAAATTA 2503 4142 TITIACAGAAATTAAAAATTITIAATAAATTAAAAAAAAAA	4342 TAÀGGÀAACAAGTGTCCTAÍTTGAÍAÍÁGCTÁCTCTAIGTTAÍTGAGTAÍGTAÍGGÍGT 43383 3217 GGTCTATATTAGTTTTGTATGATAGTCCAAGTATGTTTGTT

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TATAGAAGTIGCAATGTICGAGAGAATGCATGATAATATAACTGAGTAATATGCGATAT	\$196 CCAGITTATAATGTAGATAATTTAAGTAGTAGTAGAAGCATTATTAAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT

ATTAATTCACAGTATTTAAAAAGAGATTAAACTTTTATACTTTAGAGGTGGCGTTGGAAGAA 11039 10804 GAGGCAATTCAAAATAATATTGTATTTATAAATCTAAATTTTCCACATAATACATCTTTA 40745 40396 40864 10684 GATTTTAAATTATATGATACAGTTGATTATTACAGAAAAAATATAGAAAATATTTTAAG 40625 0395 AACGAIGGCICTACAGAIAATICCGGGGAIAICTGIGATIATIAITAGAAIAGAIGG 40336 40276 0275 AGTAGAĞCTACTĞGCGATTATATTTATTTACTTĞATTCGGATGATTATCTATATAAGAA 40216 0215 GATGCAATCGAGAGAATGGTTGAATTTAGCGAGAAATATAATTCAGAAATTTTTTAGGG 40156 10155 TGTTATGTTGAAAAAAGAGAACAACATATTATAAATATCGTTTTAGAAGATGAAATGATA 40096 :0095 GAAACTATTAGTCCAGTACAAGCAATACAAATATTTATAA---TTATGATGCCTATAGA 40039 6035 6095 6155 6215 6275 6335 6395 6455 6512 CATCGCTTTGTGGTGGCCTGTAATAAACTCTATAAAAAAGAACTATTTGAAGATTTTCGA 6686 ATGTATTATGGGAAAACTTATGGAGTTTCCCCGTTAGCAA----AATTATATCCGAGAA 40863 ATTTTAGCGATAATAGTACTACTAGGACAAAATTCAATGAGAGAATGT-TGTATTTTTTT TTGGAAAATTTGCAAAAACAAGTGATAGTATTGTTTAAGCAAATATATGGTGAGGATTTT 6096 ATAAGAATTGTTTCGAACAAAGTTTTTAAAAAAATATTATGGTTATAATAGGAAGATATC CGCATTCGTTATTTTAAAAAGAGAACGCCGGGCTATCAGATGCCCGTAATTATGGCATA AAAAATTTTATGAATTTGTATAAATAATATTTTTTTCTACTCCTGTTTGTAAACTATAT AAGAAAAGATACATAACAGATCTTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACTT GTAATTTATTGAGTAATCCATATCCAGAAGGAAAATTCATGAAGATATGGATACAACTT TITAATCTGCATTATTAAAGAATATAGATAGAGTTAGTTATTTGACTGAACATCTTTAT Traagcriaraterrecerreaaaaragcagrirereararrerecerecerer TITIATAGGAGAGGTATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCAA GACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTATAGCTTACTAATG 6156 ATGGATACTATTAGTAAATTTCTATAATTGTACCTATATAAATGTAGAAAAATATTTA 6216 TCTARARIGTATAGATAGCATTGTAARATCAGACCTACAAAACATATAGAGATTCTTCTGGTG TT---CATCCAACGTTTACACGAAGCAATTGAGAGAGAGAATGCCCTTGTGGCAGTTGCT GGTTATG-----ATAGGGTAGATGCTTCGGGGCATTTCTTAACAGCAGAGCCGCTTCCT 5976 TTTAAATACGGAAAACAGTCTATTTTGACAAATTTTTTAATTTTTTAGAAATCTTTATAAA 10564 TCCTCTATAAGATATTTCACTATTGTAAGAAAATA-----TATAATTTGAGGTTATC AAATATTATTTTAAACTTGTTAAAAGTATCTAACAAAAATTCTTTGTCTAAAAATTTTTGT 6567 ACAAATCAGGCTGTTCTGAGCGGCAGGAATGTTTGTAAAAAGCTGCTAGAGGCGGATGGT 9499 10983 5856 5916 9889 5616 5736 40923 5796 6456 6036

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975 AGTTAACCTGCTTAACTGTTGATCAAGCTTTTAATTAACATACCCATTGAATTATTTGGTA 1034
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                                 The invention relates to a protein having betal,3-galactose transferase activity, derived from a microbe having an activity of transferring galactose to N-acetyglucosamine by betal,3-bond. The protein can be used in a method for the preparation of a protein having betal,3-galactose transferase activity in which the above transformant is cultured in a medium to form and accumulate a protein having betal,3-galactose transferase activity, and in a method for the preparation of a galactose containing gluside in which a culture liquid of the above transformant or a treated product of the culture liquid of the above transformant or a treated product of the culture liquid of the above transformant or made to be present in an aqueous medium, and a galactose-containing gluside is formed and accumulated in the aqueous medium. The galactose-containing gluside is used as a candidate for infection preventors. This sequence represents DNA encoding betal,3-galactose transferase proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .035 aktaccaaatacaagatattattaatgacattgaagcaatgggagtgattgtcaatgtta 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTATTTTCGACAA 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 TATTTGAATCACATAAACAAATTCAAAAAACTCTTGTTGCATTGGTAGTTTTAGGTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                               Sequence 6865 BP; 2453 A; 847 C; 1185 G; 2380 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 917;
                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                 10.4%; Score 727.8; DB 6 59.2%; Pred. No. 6.9e-89;
     1; Page 15-22; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1389; Conservative
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40038 GCTATTTTACTGTAGCACATAATTAATTATAAGAGAGAATTATTTTCTACGCTGTGC 39979
                                                                           TATCCAGTAGGGAAGTTACACGAAGATGAATTTTTAACCTATAAATTATATTTGAAAGCC 39919
                                                                                                                                                    9918 AAAAATATAATTTTCTTTAGATATATACTTATGCATATCGTATTAGAGAAAATAGCATA 39859
                                       TITGAAAAGGGIAAGAITCAIGAAGAIGAAIACIICACIIAICGCIIGCICIAIGAGIIA 6746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betal, 3-galactose transferase; gene; ds; galactose; N-acetylglucosamine; betal, 3-bond; galactose-containing gluside; uridine-5'-diphosphate;
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product= "Betal,3-galactose
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2265. .2747
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A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis
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     TTATCCTAAGGCAATTAATTTTAGGAGGAATTTTTTAATGATTTTTTGTCACAGTAGGGACA
                                                                              TATAAAAAATTTCTCAGTTACAAAGAAATGGAACAATATATTAACAAATCAGAAGTAGTT
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Sequence 17276 BP; 5953 A; 2414 C; 3043 G; 5866 T; 0 U; 0 Other;

Query Match

10.4%; Score 726.8; DB 8; Length 17276;

Best Local Similarity 59.2%; Pred. No. 9e-89;

Matches 1366; Conservative 0; Mismatches 902; Indels 38; Gaps

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regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This sequence represents a moiety, the DNA of which can be transfected into a cell surface moiety, the DNA of which can be transfected into a cell with superantigen DNA to generate antitumour immunity.
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tumour; cancer;
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Pred. No. 9e-89;
0; Mismatches 902;
                                                                                                  Sterptococcus capsular polysaccharide DNA seq id
                                                                                                                               receptor; lipid-based tumour associated antigen; antimicrobial; gene therapy; neoplastic disease; infectious disease; capsular polysaccharide; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococci (GBS) Streptococcus agalactiae capsular polysaccharide synthesis (cps) gene in sample. The invention is useful for detecting Sagalactiae in a sample. The present sequence is S. agalactiae cps gene. This sequence is used to illustrate the method of the invention.
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This invention relates to a novel method of typing a group B streptococcus (GBS) bacterium which comprises analysing the nucleotide sequence of one or more regions within the cpsh. cpsk, cpsk, cpsk and/or cpsl/M genes of the bacterium, where the regions comprise one or more nucleotides having sequences that vary between types. The method is useful for preparing a composition for serotyping and/or subtyping a GBS bacterium for diagnosing GBS infections in pregnant women, elderly and/or immunocompromised patients. The present sequence is that of a consensus DNA sequence for the 3' end of the cpsD-cpsE-cpsF and the 5' end of the cpsG sequences of group B Streptococci which is related to the method of
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ADM79774 standard; DNA; 2226 BP

RESULT 10 ADM79774 ID ADM7 XX

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           1487 AAGAAGTCTTTTGAAGAATGAAAAATGTATCCATGTTACTTTCCAACAAATCGCAATCT
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                             CACGAGATACCAAAGTTGTTTTGATAACGAATAAGGATTCTTTTATCAAAAATGACCTTTA
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                                                                                                                              CGAAGATTGGCTCATTTATAAGACGACACTCAATT-GATGAACTGCCACAATTTATCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a fragment of the EPS plasmid derived from L. lactis subspecies cremoris Ropy352. The EPS plasmid is about 32 kb in size and encodes at least 13 active genes plasmid is about 32 kb in size and encodes at least 13 active genes plasmid is about 132 kb in size and encodes at least 13 active genes allow the bacteria to produce an exopolysaccharide, designated EPS352. When EPS352 is expressed in or added to milk, it imparts highly very thick, with a very smooth mouth-feel, and slightly sweet with an obvious chewable-bite. Open reading frames (ORF's) M and N show homology or oflycosyltransferase involved in EPS352 biosynthesis. L. lactis accession number NRRL B-30229. EPS352 is useful for thickening a liquid accession number NRRL B-30229. EPS352 is useful for thickening a liquid in and a fruit-juice. It is also useful as an additive in pharmaceutical products, beauty care products and coating agents. It is pharmaceutically, in the specification that there is an additional ORF between those encoding EpsE and Eps0. This encodes EpsF (AAB47425). However, this ORF is not indicated on the actual DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3578 TATATTTTGAAATTTAGAACAATGATTCTTAATGCCGAGCA--GTATCTAGAACTTAATC 3635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can
 CATTATCCAAAGGAAAAAACCAATTATTGTTTCCTAGACAAAAAAAGTATGGTGAACATG
                   TATTACAACTAGGTAAATTCCGATAGTTCTTCCACGCCAAATGAATTTGATGAGCATA
                                       TAAATGATCATCAA-GTAGAGTTTGTAAGAAGAATTTTTACAAGATAATAATATTTTATTT
                                                         TAAATGATCATCAACTTTGGGTAAGTAACAGGTTGTGAAAAAGGGATACTCATTGATTT
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antibacterial; drug design.
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be used to screen compounds in rational drug discovery programmes. The antiennse mucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification.
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                                                                                                                                                                                                                                                                                        Sequence 1368 BP; 412 A; 200 C; 314 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                   Score 423.2; DB 4; Length 1:
Pred. No. 5.1e-48;
0; Mismatches 548; Indels
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58.6%;
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Matches 794; Conservative
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                                                                                                                                                                                                                                                                TTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGATGA 1153
                                                                                                                                                                          1154 ATTTGAAAATATACTCCTGGTCAAAAGAGGACGATTGAGTTTTAAACCAGGGATTACAGG 1213
                                                                                                                                                                                            GTATGAGCACTATACCCCAGAACAAAAACGCCGACTAAGTTTTTAAACCTGGCATAACAGG
                                                                                                                                                                                                                                  TTTATGGCAGGTCAGCGGACGAAGTGAGATCAAGAATTTCGATGAAGTTGTCAAATTAGA 1274
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GATTCGAAAGGATGGGGGATCTGCTATTTTTGCTCAGACGCGTATAGGAAAAATGGTCG 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising a sequence
                                                                     ACTCATGGAACAAAATACCATGCAAGGTGGAATGTTT----AAGGTGGACGATGATCCT
                                                                                                          CATATITIACATICTACAAGITITCGAICGAIGTAIGTIGAIGCIGAGGAGGCGCAAAAAAGA
                                                       974 CTTGCTCAGCCAAAACCAGATGCAAGGGTGGGTATGTTTTAAAATGGGAAAAACGATCCT
                                                                                             1034 AGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGTTACCACAGTT
                                                                                                                                                      TTATAATGTTCTAAAGGGAGATATGAGTTTGGTTGGCACACGGCCACCAACAGTGGACGA
                                                                                                                                                                                                             TCTCTGGCAGGTTAGTGGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGGA
                                                                                                                                                                                                                                                     polypeptide, useful for diagnosing, preventing and/or treating
pathological conditions resulting from the bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding a Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                          ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteraemia; pneumonia; otitis media;
                                                                                                                                                                                                                                                                                          1334 GAAAGTTGTATTGTTGAGAGGGAAGTAAGTAA 1367
                                                                                                                                                                                                                                                                                                       1335 TAAAGTAGTATTTATGAGAGATGGAGCGAAGTAA 1368
                                                                                                                                                                                                                                                                                                                                                                                                                      Novel S. pneumoniae DNA sequence, SEQ ID 2303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                             ADR93668 standard; DNA; 1443 BP
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cencoding a Streptococcus pneumoniae ADR91366polypeptide, or its fragments, with any of 9 fully defined sequences (appearing as ADR94308, ADR94899, ADR94800, ADR94801, ADR94801, ADR94801, ADR94802, ADR95642, ADR95642, ADR95682, ADR96409, or any of the fully defined sequences appearing as ADR91705, ADR91986, ADR919197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or ADR931476 or at least 40 or 30 consecutive nucleotides of the nucleotide sequence. The nucleic acids and proteins are chosen from 5206 disclosed sequences. The nucleic acids and proteins are chosen from 5206 disclosed sequences. Also included are a recombinant expression vector comprising the isolated nucleic acid cited above operably linked to a transcription regulatory element, a cell comprising the recombinant expression vector and a probe sequences as cited above. The methods and compositions of the present invention are useful for the dispnosis, prevention and/or treatment of protecting and protecting from bacterial infection by the present invention are useful for the dispnosis, prevention and/or treatment of the present are accompliant and protecting are useful for the dispnosis, prevention and/or treatment of the present and a protection and conditions resulting from bacterial infection by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae e.g. pneumonia, bacterian intectious by an otitis media. The present sequence is one of the 2603 disclosed S. pneumoniae nucleic acid sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained sequence format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 AGTCTATGTGCTAAACCGATTTATCAAGTGGTATTGGAAGCGGGCTTATCCCAACTTTAA
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/note= "encodes AAY43773; this CDS, minus the termination codon, is specifically claimed (claim 6)" 12838. .13788
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS, minus the termination (claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encodes AAY43776; this CDS, minus the termination codon, is specifically claimed (claim 6)"
                                                                                                                                                                                                                              /product= "eps6; this CDS, minus the termination codon, is specifically claimed (claim 6)" fnote= "encodes AAY43772; contains a stop codon at nucleotides 9410-9412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant enzymes for biosynthesis of exopolysaccharides having e.g. antitumor or probiotic properties or useful in fermented milk products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= i
/product= "eps9"
/note= "encodes AAY43775; this CDS is specifically
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                               /product= "eps3"
/note= "encodes AAY43769"
                                                                                                                "encodes AAY43770"
                                                                                                                                                                                 /note= "encodes AAY43771"
3633. .10681
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AAX43773, AAX43774, AAY43775, AAY43776
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                                                                                               product= "eps4"
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/product= "eps7"
                                                                                                                                                                                                                                                                                                                                                                                                                  product= "eps8"
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22-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTTGAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAGGGATTACAG 1212
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                                           5305 Trangititiciacacatrititatagaraiggagaratrentesceaaacectreceara 5364
                                                                                                           rcrecesascrerastrestrestrestestestatrestaseaarcricernarecte 5424
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             TAACTITITICCACAAATTITIATAAGCCTAGTCATATCATGATGAAACGACTITIGGATA
                                                                            TACTCGGAGCGGTAGTCGGGTTATTTGTGGTATAGTTTCTATTTGTTAGTTCCAA
                                                                                                                                                                                                                                                                              973 ACTIGCICAGCCAAAACCAGAIGCAAGGGIGGGIATGTTTTAAAAIGGGAAAAACGATCC
                                                                                                                                                                                                                                                                                                                                                                     5600 ACGTATTACCAAGATTGGACATTTCATTCG-TAAAACAAGTCTTGATGAACTTCCACAAT
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                                                                                                                                              TTATTCGTAGAGATGGTGGACCGGCTATTTTTGCTCAGAAACGAGTTGGACAGAATGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eps4; eps5; eps6; eps7; eps8; eps9; eps10; exopolysaccharide biosynthesis; EPS; intersugar bond; antitumour; probiotic; foodstuff; organoleptic quality; flavour; lactic acid bacteria; acidified milk product; yoghurt; cheese; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide seguence of the eps operon of S. thermophilus Sfi39,
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/product= "eps2"
/note= "encodes AAY43768"
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3390. .4121
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6830 1201

1261 6890 1321

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EPS6;

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GACAATGATCCACGTATTACCAAAATTGGACATTTCATTCG-TAAAACGAGTCTTGATGA
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      6537 AGAAAATGGACGTATCTTCAAGTTTTATAAATTCCGTTCTATGTGTGTTGATGCGGAAGA
                                                                                AATCAAGAAGAATTTGATGGCACAGAATCAAATGTCTGGTGGTATGTTT-----AAGATG
                                                                                                                          1022 AAAAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGA
                                                                                                                                                                                                        GTTACCACAGTTTTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACC
                                                                                                                                                                                                                                                                                       TACAGTTGATGATTTTGAAAAATATATCTCCTGGTCAAAAGAGACGATTTGAGATTTTAAAACC
                                                                                                                                                                                                                                                                                                                             <u> aacagtrgargagrargaaaaararacaccrgaacagaaacgrcgrtraagrrrraaacc</u>
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EPS7; EPS8; EPS9; EPS10; Streptococcus thermophilus strain Sfi39;
activated D-galactose pyranose; saccharide; beta-glycosyltransferase;
transporter; food; fermented milk product; yoghurt; cheese;
flavour stability; organoleptic property; ss.
                                            1202 AGGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGA
                                                                                                                                                                                                                                                                                                                                                                                                               6831 TGGTATCACTGGTCTTTGGCAAGTAAGCGGTCGAAGTGAAATTACTGATTTGATGAAGT
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/product= "EPS5"
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used in foodstuffs to improve organoleptic qualities and flavour. When expressed by lactic acid bacteria, BPS impart a free-flowing character and/or a smooth, creamy texture to acidified milk products (yoghurt or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6297 TAATTTGAATGCCCTTGAATTTATGAATCAAGGTGAAAAACGTATTCAACAATTGGGTCC
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                                                                                                                                         Score 376.2; DB 3; Length 19966;
Pred. No. 9.2e-42;
0; Mismatches 593; Indels 18;
                                                                                                     Sequence 19966 BP; 6405 A; 3133 C; 3732 G;
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al Similarity 56.1%;
780; Conservative (
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2 TCGCCAAACGAAATTGGCATTATTTGATATGATAGCAGTTGCAATTTCTGCAATCTTAAC

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The present sequence encodes enzymes involved in the biosynthesis of exopolysaccharides (EPS). These enzymes are designated EPS1-EPS10. and are encoded by open reading frames eps1-eps10. The enzymes are isolated from Streptococcus thermophilus strain Si139. The proteins are used in a method for the synthesis of EPS, which includes at least one step of forming a bond (alpha or beta-isomer) between C-1 (carrying the reducing aldehyde function, of an activated D-galactose pyranose), and a phosphate on a lipophilic or proteinaceous primer. Stepwise synthesis of EPS occurs with, in each step, addition of a new sugar unit, through its hemi-acetyl function, to an alcoholic hydroxyl of a second sugar unit, present at the cond of a chain of sugar residues bonded to the primer. EPS1 to EPS4 are used to elongate the EPS chain, and to regulate EPS production, EPS5 creates new bonds between saccharides, EPS6 is used in the biosynthesis of EPS, EPS7 and EPS8 are beta-glycosyltransferases, EPS9 is a transporter of repetitive units, and EPS10 catalyses the conversion of a pyranose form of a beta-D-galactose to the furanose form. The EPS enzyme or properties of foods, particularly fermented milk proporties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant enzymes for synthesis of exopolysaccharides, particularly in lactic acid bacteria, for improving properties of fermented milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products such as yoghurt and cheese, e.g. their organoleptic properties and flavour stability
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                                                             /note= "encodes AAY54070; contains 1 stop codon nucleotides 9410-9412"
                                                                                                                                                                                                                                                                                                                                               "encodes AAY54074"
"encodes AAY54069"
                                                                                                                                               /note= "encodes AAY54071"
[2838. .13788
                                                                                                                                                                                                                                                                              /note= "encodes AAY54073"
16919. .18016
                                                                                                                                                                                                              /note= "encodes AAY54072"
14138. 15553
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AAX54071, AAX54072, AAY54073, AAX54074.
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/product= "EPS10"
/note= "encodes AJ
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                                               product= "EPS6"
                                                                                                                               "EPS7"
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22-APR-1998;
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                                       62 AAGTCATATACCAAATGCTGATTTAAATCGTTCTGGAATTTTTATCATAATGATGGTTCA 121
                                                                                                                      122 TTATTTTGCATTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGAT 181
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5649 ICGICGCAIIGAAATIGGIAITAIACAGIIGGIIGGIIGIIGIITITCGCAGCCAIGGIAGC
                                                                            5709 TAGTAAAATACCATATACAGAGATTACCCAAGGAAGCATTGTCCTTTTAGGTGTCGTACA
                                                                                                                                                           5769 TGTAGTGTCTTACTATATCAGTAGTTATTATGAAAATCTTAAGTATAGAGGCTACTTGGA
                                                                                                                                                                                                                                          829 IGAACTCATTGCAACTGTCAAATATTGTTTCATATTGCTCTAATTGTAACATTTCTCTC
                                                                                                                                                                                                                                                                                 242 ATTTTTGTTGGAGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAAT
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Query Match 5.4%; Score 376.2; DB 3; Length 19966; Best Local Similarity 56.1%; Pred. No. 9.2e-42; Matches 780; Conservative 0; Mismatches 593; Indels 18;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
                                                                                                                                                                                                                                                                                                                               product;
                                                                                                                                                      AGGGATTACAGGTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGT
                             TACAGTTGATGAATTTGAAAATATACTCCTGGTCAAAAGAGAGGACGATTGAGTTTTAAAACC
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Length 28170;

Score 376; DB 6; Length 281 Pred. No. 9.7e-42; 0; Mismatches 580; Indels

Query Match 5.4%; Best Local Similarity 56.7%; Matches 782; Conservative

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                                                                                                                                  GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTGGTTCGGTTGG
                                                                AATTTGAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAAACCAGGGATTACAG
TTTATAATGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGATG
                    TTTGGAATGTTCTAAAAAGGTGATATGAGCTTGGTAGGAACACGTCCACCAACATGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
                                                                                                                       ACGITGCITATITGGACGGATGGACAATCIGGCGCGCGATATIAAAATCTIATIGAAAACAA
                                                                                                                                                                                                                                                                TTAAAGTAGTAATGAAGGATGGAGGAAAGTGATGGCTTTCTCCATTTCTTTTAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exopolysaccharide; lactic acid bacterium; eps; fermented food product;
TTTGGAATGTTCTAAAAGGTGATATGAGCTTGGTAGGAACACGTCCACCAACATTGGATG
                                                                AGTACGAATCTTATACACCGGAACAAAAACGTCGCCTCAGCTTTAAACCAGGTATTACTG
                                                                                                  GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGG
                                                                                                                                                                   ACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTTAATAAAGACAG
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                                 AATTTGAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAAACCAGGGATTACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid fragments containing exopolysaccharide operon, useful for increasing exopolysacchride synthesis in lactic acid bacteria
                                                                                                                                                                                                                                                                                    fermented food product;
AACATTGGATGAGTACGAATCTTATACACCGGAACAAAAACGTCGCCTCAGCTTTAAACC
                             AGGGATTACAGGTCTCTGGCAGGTTAGTGGTGGTAGTAATATCACAGACTTCGACGACGT
                                        AGTICGGITGGACTIAGCATACATIGATAATIGGACTATCIGGICAGATATIAAAATTIT
                                                                                 reraaacragacarrecrrarargeacgargeacaarcregcergararcaaaararr
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TACAGTTGATGAATTTGAAAATATACTCCTGGTCAAAAGAGAGGATTGAGTTTTAAACC
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TACAGTTGATGAATTTGAAAATATACTCCTGGTCAAAAGAGACGATTGAAACC
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                                                                                                    AGTICGGTIGGACTTAGCATTGATAATTGGACTATCTGGTCAGATATTAAAATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria
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                                           AATTTGAAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAGGGATTACAG
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CTTATACAGAGATTACCCAAGGAAGCATTGTCCTTTTAGGTGTCATACATGTGTGTCTT
                                                                      TTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATAGAGTTTGAAA
                                                                                                                                                                                                        AAACATTTAACTATAGTATATATTTGCAATTTTTCTTACGGCAGTATCATTTTTGTTGG
                                                                                                                                                                                                                                                                                                                                         AGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAATATGCAAGTTT
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    --GTTTTGTCTCGTATGAAGACAATATGGATGGTAGGATTACAGCAGTTTGTGTTTTGG

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                                                                                       4769 TTTTTTGCAGATGGGAAGTTTTTCAATCTCACGTCGCGGACTTCTTTACGTCACCATGATT
                                                                                                                                                                                            1829 TCAGGTGTTCTCTTATACGTTACAATACTGTTCTTAAGTATTTCCGCTCATCTATTTAT
                                                                                                                                                                                                                                                                                                          1889 ACACGTCGTAAAAGTAACAAGAATATTCTCTTGATTTCTGATCAGGCACGTCTTGATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 TTAGGTACAGAAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAA
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                                       TTTTTGTTGGAGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATA
                                                                                                                                          AACTTCGTTTTGGTATACCTATTTAACGTAATTATTAAGCAGTTTAAGGATAGCTTTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an eps operon from Streptococcus thermophilus. Proteins encoded by the eps operon function in exopolysaccharide (EPS) synchhesis. The operon is useful for producing chimeric eps operons, for optimising production of EPS in lactic acid bacteria. EPS impart texture, mouth feel and theological properties to fermented food products (e.g. yoghurt). They function as thickeners, to provide free-flowing and creamy texture, and may also have biological activities beneficial to health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTTTGCATTTTTTATATCTCGTATGCCAGTTGAATTTGAGTATAGAGGTAATCTGATA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid fragments containing exopolysaccharide operon, useful e.g. for increasing exopolysacchride synthesis in lactic acid bacteria.
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GTCTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAGTTCGGTTGG
                                                                                                                              GTCTTTGGCAAGTAAGCGGTCGAAGTGAAATTACTGATTTTGATGAAGTTGTAAACTAG
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                                                                                                                                                                                                                           TGAAAGTTGTATTGTTGAGAGAGGGAAGTAAGTAAAAGTATATGAAAGTTTGGTTGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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57.2%; Pred. No. 1.1e-37;
ive 0; Mismatches 529; Indels
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(DANO-) CIE DANONE SA GERVAIS.
(RHOD ) RHODIA CHIM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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Best Local Similarity 57.2
Matches 727; Conservative
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Search completed: April 29, 2005, 02:36:47 Job time : 3285 secs

Sequence 26,

Sequence Sequence Sequence

Perfect score:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

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Sequence 3, Application US/09900038A
; Patent No. 6828128
; Fatent No. 6828128
; GENERAL INFORMATION:
    APPLICANT: Miyake, Katsuhide
; APPLICANT: Miyake, Katsuhide
; APPLICANT: Iljima, Shinji
; APPLICANT: Iljima, Shinji
; TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the same
; TILE REFERENCE: 766.53
; CURRENT APPLICATION NUMBER: US/09/900,038A
; CURRENT APPLICATION NUMBER: US 2001-09-21
; PRIOR APLICATION NUMBER: JP 2001-392
; RIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
: LENGTH: 6865
 Sequence 199, App
Sequence 199, App
Sequence 29, Appl
Sequence 12776, A
Sequence 15940, A
Sequence 15940, A
Sequence 26, Appl
Sequence 26, Appl
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                                                                                                                                                                    Sequence 12776,
Sequence 15940,
Sequence 1, Appl
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                                                                                                                                                                                                                                                                      Sequence Sequence
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Pred. No. 3.7e-122;
0; Mismatches 917;
US-08-961-083-199
US-09-536-784-199
US-09-634-238-97
US-09-949-016-15940
US-09-949-016-15940
US-09-816-028A-26
US-10-303-152-26
US-10-303-134-26
US-09-949-016-12776
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US-09-949-016-0288-30
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NAME/KEY: CDS
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LOCATION: (5009)..(5947)
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NAME/KEY: CDS
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Sequence 1469, Ap
Sequence 14164, A
Sequence 1006, Ap
Sequence 893, App
Sequence 2107, Ap
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
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                                                                                                                 April 27, 2005, 21:09:50 ; Search time 1097 Seconds (without alignments) 10429.213 Million cell updates/sec
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Sequence 2303, Ap
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Sequence 2987, Ap
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cgn2_6/ptodata/1/ina/5A_COMB.seq:*

cgn2_6/ptodata/1/ina/5B_COMB.seq:*

cgn2_6/ptodata/1/ina/6A_COMB.seq:*

cgn2_6/ptodata/1/ina/6B_COMB.seq:*

cgn2_6/ptodata/1/ina/ReZOMB.seq:*

cgn2_6/ptodata/1/ina/ReZIMS_COMB.seq:*
                    5.1.6
Compugen Ltd.
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US-09-134-000C-2987
US-09-134-000C-2344
US-09-107-532A-1469
US-09-949-016-14164
US-09-948-039A-1006
US-09-949-016-14164
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US-09-949-016-17067
US-08-961-527-86
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                                                                                                                                                                                                                                                                                                       1202784 seqs, 818138359 residues
                    version :
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                    GenCore (c) 1993 -
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seq length: 200000000
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS
THERAPEUTICS
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
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STATE: Massachusetts
COUNTRY: USA
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CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-05-12
PRIOR FILING DATE: 1997-07-02
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58.3%; Pred. No. 5.5e-66;
ive 0; Mismatches 552;
                                                                                                                                                                Sequence 1332, Application US/09583110
Patent No. 6699703
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2769 AATTGAA 2775
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US-09-583-110-1332
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                                         614 AAAGCAATTCGTTTCAGATTTTTGAGTTGTTAGGTATTGATGTAAGCGTTGATATTC
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; Patent No. 6506581
; GENERAL INFORMATION:
    APPLICANT: Fleischmann et al.
    TITLE OF INVENTION: the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus influenzae in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the Haemophilus in the
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CORRESSPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-557-884-1
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Best Local Similarity 58.3%; Pred. No. 5.5e-66;
Matches 789; Conservative 0; Mismatches 552;
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-0un-1998
PRIOR APPLICATION NUMBER: 60/085131
APPLICATION NUMBER: 60/05153
FILING DATE: May 12, 1999
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature

LOCATION: (B) LÖCATION 1...1443

SEQUENCE DESCRIPTION: SEQ ID NO: 2303:

US-09-107-433-2303
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMPUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2303:
SEQUENCE CHARACTERISTICS:
LENGTH: 1443 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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924401 AATCTGGCTAAACTATCTTCTCGTATTTTGAAACGAACCATGGATATTGTTGTTGGTTC 924460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 AATTTTTATAAGCCTAGTCATATCATGATGAAACGACTTTTGGATATACTCGGAGCGGTA
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     1340 TGTATTGTTGAGAGAGGAAGTAAGTAAAAGTATAT 1375
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Pred. No. 6.7e-19;
); Mismatches 266;
                                                       924997 GGTTTTAAATCGTGATGGAGCTTATTAACGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/643,990A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                           Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide s
the Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/487,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                   APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                   Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 301-610-5790
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                         Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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Best Local Similarity 56.4%;
Matches 359; Conservative
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STATE: MD
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                                                                                                                                                          US-09-643-990A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124701 ACTABABATCGGTGCTTTTATTCGC-AAAACAAGTTTAGATGAATTACCTCAATTATTTAA 924759
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Pred. No. 6.7e-19;
                                                                                                                                                                              APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 084476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INPORMATION:
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
                                                                                                                                                                                                                                                                                                                                                                    NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                      OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.3
Best Local Similarity 56.4
Matches 359; Conservative
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1851 ATTCTCTATAAATAATATTGATTTAGTCACAAGATTGGAGAATTACCCCTTTAAGTTAAA 4910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4671 GTGCAAGCTTTATTCACGAGATATTATAAAGATATAAAATTCCAAATTAATAATAGAAG 4730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 TGATGGATCTCCTGACAATAGCGGGAAAATCTGTGATGAGTATGCTGAAAAAGATAATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAATATAARGIGIGAGATTAGTATTATTGTTCCTGTGTATAAAGTTGAAAAATATTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1311 TGATGGAAGTACTGATGATTCTGAAAAATTTGCTTAAACTATATGAAGAACGATGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 TGTTGCGAGAGGCAAATACTTAGGCTTTGATGACAGTGATGATTATTATTGATGAAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGAGAGAGAGACTGTAAAAGAATTTTTGTCAGGATCTAATATAGAAAATAATGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 AAATAAAAGGAAGCAATAAAATCTGTTTTAGAAGGAACGCAATTTTATGCATACGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1731 TATTGGTGAGGATTTGCTTTTTAATTTGGAGGTCTTGAACAATGTAACACGTGTAGTAGT
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                           Length 984;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                      Score 152.6; DB 4;
Pred. No. 1.6e-18;
0; Mismatches 354;
                                                                                                                                                    NAME/KEY: misc_feature;
; LOCATION: (B) LOCATION 1...984;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2527:
US-09-107-532A-2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAGAGTTTAGTCATTATTTTGATGC 4937
                                                                                                                          ORGANISM: Enterococcus faecium
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; Patent No. 6617156
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ULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                        Query Match 2.2%;
Best Local Similarity 51.4%;
Matches 384; Conservative
                                                     HYPOTHETICAL: NO
                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-134-000C-2987
                                  MOLECULE
                                                                                                                                                FEATURE
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
924820 GCGTTATGAAGAAAACGTAGATTATTACTTAATGGCAAGACCCGGTATGACAGGGCTTTG 924879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924880 GCAAGTCAGCGGACGTAATAATATTC---GATTATAATACTCGCGTTTATTTTGATTCTTG 924936
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                                                                                                                       924641 GATCCTGAAGCAAGACTGAATGGGAAAAAGATTTTAAATTAAAGAATGATCCTAGAATT
                                                                                                                                                                      1040 ACTCCAATTGGACATTTCATACGCAAAAACAAGTTTAGACGAGTTACCACAGTTTTATAA
                                                                                                                                                                                                                                                                  TGTTTTAATTGGCGATATGAGTCTAGTTGGTACACGTCCACCTACAGTTGAATTTGA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1340 TGTATTGTTGAGAGGGGAAGTAAGTAAAGTATAT 1375
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09107532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2527:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 984 base pairs
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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Patent No. 6583275
GENERAL INFORMATION:
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
SOFTWARE: PATENT IN VERSION 3.1
SEQ ID NO 2987
LENGTH: 993
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.1%; Score 145.4; DB 4; Length
Best Local Similarity 52.0%; Pred. No. 3.2e-17;
Matches 382; Conservative 0; Mismatches 341; Indels
                                                                                                                                                                                                                                                                                                                                , ORGANISM: Enterococcus faecalis
US-09-134-000C-2987
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Sequence 71, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6452
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                                                                                                                                                                                                                                                                               ZIP: 20030
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: AYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 144.6; DB 3;
52.3%; Pred. No. 9.1e-17;
tive 0; Mismatches 329;
                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPAK: (301) 309-8514
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32768 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1'
Best Local Similarity 52.3
Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: ASCII Te
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US-08-961-527-71
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385 TTTTCTTCTGAAGAAGAGTTGAGCGAGATATATTATGGCAATATATCCGATAAATACAAT 444
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  TGATATTGCAGTTGGTAATTATTATTCTTTCAACGAAAGTGAAGGAATGTTCTACTTTCA 6572
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTERCOCCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1999-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
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                                                                             TATATTGGGAGACTCCTATTATGAGAAGTATATGATAATGTTTCTATCTTTGAGAACTT
                                                                                                                                                                                                           GAAAAGATACATAACAGATCTTTTTCAAGAATCAATGGTTAGGAGAAGATTTACTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                             TTATCGGATTAGAAAGGTAGTTTATCAAGAGTTTGGACAGAA 6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2344, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
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Sequence 11114, Application US/09949016
Patent No. 6812339
GRNERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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  309 TGATGAAGATATGTATGCATTTTTATATAACAATATATTGAAATATGAGGGGGTTATC 368
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                                                                                                                                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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1451 ATGATAAATTATTTATTAGAATACATCAAAGAAAATAACTTGGTAAACTTAGAACAAT 1510
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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Best Local Similarity 48.0%; Pred. No. 9e-16;
Matches 480; Conservative 0; Mismatches 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1002
; SEQUENCE DESCRIPTION: SEQ ID NO: 1469:
US-09-107-532A-1469
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REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                       Sequence 1469, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                       STREET: 100 Beaver Street
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LENGTH: 1002 base pairs
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MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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                                          TTTTTCAAGAGAAT
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US-09-107-532A-1469
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; Sequence 1006, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Klebgiella pneumoniae
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                                                                                                                                                                                                     2910 TGATGAATTGCTAAATGCAAGAAATTTAGGTTTTTTTTTGCTAGAAAGTTAAAATAGA
                                                                                                                                            16;
                                                                                                                          Length 18773;
                                                                                                                       Score 132.6; DB 4; Length
Pred. No. 1.2e-14;
0; Mismatches 659; Indels
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14164
                                                                                                                       Query Match 1.9%;
Best Local Similarity 47.2%;
Matches 604; Conservative
                                                                                TYPE: DNA
ORGANISM: Human
                                                                                                    US-09-949-016-14164
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
17312 TATATTAAATAATATTTTTTATATGTTATATTATATACATTATTAGATATTCTATATA 17253
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                                                                                                3748 TATTTGTAATACTACTTATTATTAAATACTGAATTGCTTTACCATGAAATTTTGGCTG
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1.9%; Score 132.2; DB 4;
Best Local Similarity 54.1%; Pred. No. 8.5e-15;
Matches 340; Conservative 0; Mismatches 278;
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GTATATATATATATATATATATATATATATATACAATATATATATATATATATATATATATATA 17635
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                                                                                                 ATTITATACATAATTATTAATTATATAATTAATATATAATATATC----TTATACATAA
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Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: PESESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                 GGCAGGTGAGCGGGCGTAGTGTC---GATTATGATACTCGTGTGTACTTGGATGCGT 1432
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TACTCCAATTGGACATTTCATACGCAAAACAAGTTTAGACGAGTTACCACAGTTTTATA
                                                                           TACTAGTATTGGTCATTTTTTACGTA-GGACAAGTTTGGATGAACTTCCTCAATTGTTCA
                                                                                                                                                                                AAAAATATACTCCTGGTCAAAAGAGACGATTGAGTTTTAAACCAGGGATTACAGGTCTCT
                                                                                                                                                                                                               AGCGATATAACGATGAGGTCGACTACTATCTATTAAGTAAACCTGGGATGACTGGGCTAT
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Pred. No. 4.9e-14;
0; Mismatches 708; Indels
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Matches 595; Conservative
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FOR DIAGNO.

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6293 TAATTCGGAAGAAATTTGTTTAGCATATGCGAAGAAAGATAGTCGCATTCGTTATTTAA 6352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 TAAAAAGAACGAAGGATTGTCGCAAGCACGAAATGATGGGGATGAAGCAGGCTCACGGGGA 263
                         Sequence 2107, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AATTAGTGTGATTGTGCCAGTCTATAATGTGCCCCAGTACCTAGAAAATCGATAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                       GENOME THERAPEUTICS CORPORATION
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Pred. No. 5.8e-14;
0; Mismatches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...996
SEQUENCE DESCRIPTION: SEQ ID NO: 2107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                   THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 996 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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Best Local Similarity 51.2%;
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
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JS-09-107-433-2107
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                                                                  Patent No. 002070.2

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE OF INVENTION: Pheumoniae for Diagnostics and Therapeutics
FILE OF INVENTION: Pheumoniae for Diagnostics and Therapeutics
FILE OF INVENTION: NUMBER: US 09/953,110
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127.4; DB 4; Length
Pred. No. 5.7e-14;
0; Mismatches 306; Indels
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                      Sequence 893, Application US/09583110
Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%;
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Matches 327; Conserv
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APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thoman B.
APPLICANT: Wellems, Thoman B.
APPLICANT: ALINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
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ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
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TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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TOPOLOGY: li
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                                                                                                           Score 125.8; DB 2;
Pred. No. 2e-13;
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Best Local Similarity 42.5
Matches 1421; Conservative
HYPOTHETICAL:
; ANTI-SENSE:
US-08-487-826B-13
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TTATTCTATCGTATAAAATTAAAATTTATTATAAATTAAACAAATTAGAAAAAAATTTAG 4048
                                                                                      ATATTTTATTATTATATACTTTTTTATAATACAATAAATATTCAGATTCTAATGAGGAA 3988
                                                                                                                                           TATTATGGTTATAATAGGAAGATATCATGGATACTATTAGTAAAATTTCTATAATTGTAC 6189
                                                                                                                                                                                            3987 ATATATATTTGTATAATGGAAAGCTAATGGTGCCATATTAAAAAATTATAATAACAACTT 3928
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                                                  AAAATTCTTTGTCTAAAAATTTTTGTATAAGAATTGTTTCGAACAAAGTTTTTAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17657, Application US/09949016

Fatent No. 681239

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

FRIOR PELLING DATE: 2000-10-20

FRIOR PELLING DATE: 2000-10-03

FRIOR PELLING DATE: 2000-10-08

FRIOR PELLING DATE: 2000-10-08

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FRIOR FILIN
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                                                                                                                                                                                                                                            CTA-TATATATGTAGAAAATATTTATCTAAATGTATAGATAGCAT 6235
                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(95255)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17067
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LOCATION: (1)...(95255)
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ORGANISM: Human
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Best Local Simil
Matches 903; C
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13449 CAATTCTATGTTATATCATACTTTGTATATATATACAATTCTGTTATATCATATTTGT
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                                                                                           2649 ATAGAATAAAAACATGGTCTAAGAATAAGATTTGGTTCTAATTGGGTTTCGCTTCCACA
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Sequence 1, Application US/08597236; Patent No. 5733765; GENERAL INFORMATION:
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IBM PC compatible
                                                                                                Conservative
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-86
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                               Local Similarity
Les 325; Conserv
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                              42082 ITTGTATATGATATAGAATTATAATTCTATGTTATATTTTGTATATGAATTATA 42023
 12142 TGTATCTAATATATAATTCTATATTATATTTTGTATCTAATATATTCTATGTTATAT 42083
                                                                                                                                                                                                                                                                                           AATTTGCTTGGATAAAAAGCTAATAGTAATATTTGTAATACTACTTATTATTTTAAATA 3777
                                                                                                                                                              3838 CTAGATTTATTATTATCAAGGAAGTATTGATAAGGTATTAGAAAACAATATTTTATTTG 3897
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                                                                                              CTGAATTGCTTTACCATGAAATTTTGGCTGTTTATAATTCTAGAGAATCAAGTAACGAAG
                                                                                                                                                                                                                                                                                                                          ZIF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486,33
OPERATING SYSTEM: MSDOS version 6.2
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Patent No. 6420135
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340
TELEDHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 19390 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1162 TCAAACATTTCTAAAGGAATACCTCATAGGTGAAAAAATACCTGGGACGATTTGCAATAA 4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6653 ACTCTATAAAAAAGAACTATTTGAAGATTTTCGATTTGAAAGGGTAAGATTCATGAAGA 6712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4102 GCTAATCAAGAGACAGATTGCAACTGCCCTATCCTTTTCCTAAGGGGTTGATTTACGAAGA 4043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAATACTTCACTTATCGCTTGCTCTATGAGTTAGAAAAAGTTGCAATAGTTAAGGAGTG 6772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4042 reccrárraccarrirraarrinaarcaagruseccaagaagrareregruaaracraaacc 3983
                                                                                                                                                          4516 CATTCAGAAGCAGACCTATCAAAATCTGGAAATTATTCTTGTTGATGATGGTGCAACAGA
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                                                                                                                                                                                                                                                                                                            6233 CATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTGGTGAATGACGGTAGTACGGA
       Length 19390;
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                                                                              Indels
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1.8%; Score 124.2; DB 3;
50.9%; Pred. No. 4e-13;
iive 0; Mismatches 308;
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APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                        CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRAUCAI A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 6425..7540
OTHER INFORMATION: /product= "epsG"
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OTHER INFORMATION: /product= "epsM"
FATURE:
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LOCATION: 1807..2535
OTHER INFORMATION: /product= "epsB'
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OTHER INFORMATION: /product= "epsD'
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LOCATION: 4898..5854
OTHER INFORMATION: /product= "epsF'
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LOCATION: 8221..9192
OTHER INFORMATION: /product= "eps!"
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OTHER INFORMATION: /product= "epsK'
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OTHER INFORMATION: /product= "epsA
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
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LOCATION: 2547..3239
OTHER INFORMATION: /product=
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LOCATION: 9285..10364
OTHER INFORMATION: /product=
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NAME/KEY: CDS
LOCATION: 7736..8212
OTHER INFORMATION: /product=
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LOCATION: 4051..4731
OTHER INFORMATION: /product=
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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10392..11339
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LOCATION: 11302..12222
OTHER INFORMATION: /prc
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6177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cactiticaatatgegaaaaatitgitaatcaggataaaagatititititataaag
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                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                      Length 14602;
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Pred. No. 8.6e-13;
0; Mismatches 358; Indels
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NAME/KEY: misc_feature
LOCATION: 13732..14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product= "orfz"
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; Sequence 1, Application US/08746682A
; Patent No. 5786184
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.5%;
Matches 337; Conservative
                                                                                                                       terminator
                                                                                                                                                                                promoter
274..302
                                                                                                                                           230..252
                                                                                                                                                                                                                                                          340..345
                                                                                                FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:

US-08-597-236-1
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STATE: New York

COUNTRY: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION NUMBER: 08/597,236
FILING APPLICATION NUMBER: EP 95201669.9
FILING APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: 20-JUN-1995
APPLICATION NUMBER: 30.56
INFORMATION FOR ESO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
INFORMATION FOR ESO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14602 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde
STREET: 1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 8221..9192
OTHER INFORMATION: /product= "eps!"
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LOCATION: 352..1803
OTHER INFORMATION: /product= "epsA"
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LOCATION: 2547..3239
OTHER INFORMATION: /product= "epsC"
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LOCATION: 4898..5854
OTHER INFORMATION: /product= "epsF"
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LOCATION: 6425..7540
OTHER INFORMATION: /product= "epsG"
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OTHER INFORMATION: /product= "epsB"
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OTHER INFORMATION: /product= "epsD'
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LOCATION: 4051..4731
OTHER INFORMATION: /product= "epsE'
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OTHER INFORMATION: /product= "epsH"
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MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                              CITY: New York STATE: New Yor!
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8483 ICACATTICIAGAIAGIGALGACIACAIAGIAAAAGAITAICITICICATTIGGIAGCIG 8542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5238 TAAATCAGACCTACAAACATATAGAGATTCTTCTGGTGAATGACGGTAGTACGGATAATT
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                                                                                                                                                                                                                   LOCATION: 11302 12222
OTHER INFORMATION: /product= "CDS (eps L) covering CDS
OTHER INFORMATION: (eps k) on nucleotides 10392-11339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.7%; Score 122.2; DB 1; Length
Best Local Similarity 48.5%; Pred. No. 8.6e-13;
Matches 337; Conservative 0; Mismatches 358; Indels
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 13732..14305
OTHER INFORMATION: /function= "CDS on the
OTHER INFORMATION: complementary strand"
OTHER INFORMATION: /product= "orfz"
FEATURE:
NAME/KEY: CDS
LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
                                                                                                                        LOCATION: 10392..11339
OTHER INFORMATION: /product= "epsk"
EATURE:
                                                                                                                                                                                                                                                                                                                                              LOCATION: 12233..13651
OTHER INFORMATION: /product= "epsM"
                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terminator
230..252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
274..302
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                                                                      FEATURE:
NAME/KEY: CDS
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NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
US-08-746-682A-1
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5773 CACAATGAAAAAACTTAGGTCTTTAAGAGCAAGATATGAAGGTGTGAAAGTAGCAAAC 5714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
FILE REFERENCE: 019633-0001110S
CURRENT APPLICATION NUMBER: US/09/816,028A
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR RAPLICATION NUMBER: US 09/495,406
NUMBER OF SEQ ID NOS: 49
TICCAGCAATAATAACTITITICAIGATTATITICCAICAAGATTTATITAACGATTT
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                                                                                              TTATATTTTAATATTATAAAAGTAGAAGTGATTTATCTGGT-TGTTTGTACGCTACTTT
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                                                                                                                                                                                                                        TTCAGAAAATATATAATTTTTGAAGTGAATAATCCAAATATTTGATTTTTGA
                                                                                                                                                                                                                                                                                      TGAAAGTAATGTTATTTCATATAAAAGTTTGACTTTAATTCTGGTTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384; OTHER INFORMATION: including LOS biosynthesis locus US-09-816-028A-1
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Pred. No. 1.1e-12;
0; Mismatches 261; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09816028A; Patent No. 6699705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Campylobacter jejuni
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Best Local Similarity 54.8%;
Matches 324; Conservative (
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APPLICANT: Gilbert, Michel
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SEQ ID NO 1
LENGTH: 11474
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US-09-816-028A-1/c
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                                ATAAAAAAGAACTATTTGAAGATTTTCGATTTGAAAAGGGTAAGATTCATGAAGATGAAT
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APPLICANT: Mational Research Council of Canada
APPLICANT: Mational Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for B
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-00010US
CURRENT APPLICATION NUMBER: US/09/495,406
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                          Score 121.4; DB 4;
Pred. No. 1.1e-12;
0; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09495406
Patent No. 6503744
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ORGANISM: Campylobacter jejuni
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Best Local Similarity 54.8%;
Matches 324; Conservative
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APPLICANT: Gilbert, Michel
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OTHER INFORMATION:
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US-09-495-406-1/c
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APPLICANT: Gilbert, Makarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Wational Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019533-000111US
CURRENT APPLICATION NUMBER: US/10/303,134
CURRENT FILING DATE: 2002-11-21
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                                                               5713 TCTCCTTATATATGTTTTTTAGATCCTGATGATTATTTGGA-ACTAAATGCTTGTGAAGA
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OTHER INFORMATION: including LOS biosynthesis locus
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                                  5415 GCTGAATATATGTTTGTTGACTCTGATGATGTTGTT
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PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FLING DATE: 1999-02-01
PRIOR FLING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.1
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Patent No. 6825019
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GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Waterchuk, Warren W.
APPLICANT: Waterchuk, Warren W.
APPLICANT: Waterchuk, Warren W.
APPLICANT: Waterchuk, Warren W.
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
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TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases of
TITLE OF INVENTION OWBER: US/10/303.162
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 1999-02-01
PRIOR PRIOR APPLICATION NUMBER: US 09/495,406
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARRE: Patentin Ver. 2.1
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                                                                              TTATATTTTAATATATAAAAAGTAGAAGTGATTTATCTGGT-TGTTTGTACGCTACTTT 5533
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1.7%; Score 121.4; DB 4; Length 11474;
Best Local Similarity 54.8%; Pred. No. 1.1e-12;
Matches 324; Conservative 0; Mismatches 261; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 11.5 kb PCR product from C. jejuni OH4384
OTHER INFORMATION: including LOS biosynthesis locus
                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10303162
Patent No. 6723545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                     US-10-303-162-1/c
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 3804 AGAACTTCATTTTTATTGTTATATATAAAATAAGAAATTTGAAAAGTAATTTAC 3863
                                                                                                                                                                                                                                                                                                                                                                                             <u> 3984 АТАГТТССТСАТТА--GAAТСТGAAТАТТТАГТАТТАТАТАААААААAATATTATAATA 4041</u>
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APPLICANT: Wellems, Thomas B.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 119.2; DB 2;
Pred. No. 3.2e-12;
0; Mismatches 1983;
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620 Newport Center Drive 16th Floor
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PILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSON NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
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TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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nucleic acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Ma.
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5255 9009 5435 6195 5555 6255 6615 5956 5556 GAAGTGAATAATCCAAATATTGAAGCAATTAATACCGTGCAGGACATGGGAGAA 5615 5914 T-CAAGAAAGCATTTAGTTACGTTGTATTTGATGAAATTTTCGCCTAAACTATATGTAAT 5135 5780 İGCATTACAĞTTAAGGGİTTATAGİTTİTİTİTTİTTİTİTTGTACATATATATAAAAH 5839 5316 TGCAAGGAATATGCAGAAAAAGATAAAAGAGTAAAAATTTTTTCACTAATCATAGTGGA 5375 5436 GACTCTGATGATGTTGATAGTAGATTAGTAGAAAAATTATATTTTAATATATATAAAA 5495 6316 TTTTACTTATTTTTTTTTATACATAAATTTTGAAATTCATAAAATGCATGAAATA 6375 s616 aaatatgatagataatatagatagagagaaacgaagaacatattitgtererritgttate 6675 5975 GITTAAATACGGAAAACAGTCTATTTTTGACAATTTTTTAATTTTTAGAAATCTTTATAA 6034 6035 AAAATATTTTTAACTTGTTAAAAGTATCTAACAAAAATTCTTTGTCTAAAAATTTTTG 6094 6736 ATGTTAATAATTAAATATATAAACACGTTGCATATATACTTTTTTTATATGTTTGTATTTT 6795 5095 TATAAGAATTGTTTCGAACAAGTTTTTAAAAAATATTATGGTTATAATAGGAAGATAT 6154 5675 TAAGAAAAGATACATAACAGATCTTTTCAAGAGAATCAATGGTTAGGAGAAGATTTACT 5734 TITITATAGGAGGGTATACTAAGTACAGTAAATTCTTTTAAAGAAGGTGTGTTTTTGCA 5854 6496 artratrarahartratrararahakahacahahararahahahahaharaharahartrar 6555 5915 TGACGTATCAATTGTTAAAGATACTATACGTTGGCAAGTATTTTATTAGCTTACTAAT 5974 5196 CCAGTTTATAATGTAGATAAATATTTAAGTAGTTGTATAGAAAGCATTATTAATCAAAAT 5900 TATATATAA---GACATTAAAACTATACTAATAGGTAATTAGTTTTATTATATATCATCT 5256 TATAAAATATAGAAATATTATTGATAGATGATGGCTCTGTAGATGATTCTGCTAAAATA 6136 TACTATTTTATACATGCATTTTTATATATTTTAGTATATACTTTAAAGATATTAATT 5496 AGTAGAAGTGATTTATCTGGTTGTTGTACGCTACTTTTTCAGAAAATATAATTTT 6196 ATTTATATAGTAGCATATATGTATTTATATAACAAATATTTTCATTTATATAATAT 5855 ATTGGAAAATTTGCAAAAACAAGTGATAGTATTGTTTAAGCAAATATATGGTGAGGATTT 5795

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6213 TTATCTAAATGTATAGATAGCATTGTAAATCAGACCTACAAACATATAGAGATTCTTCTG 6272
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Sequence 83, Appl
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Sequence 83,
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(cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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(cgn2_6/ptodata/1/pubpna/DS08_NEW_PUB.seq:*
(cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-870-759-83

US-09-751-708A-83

US-10-428-817A-79

US-10-192-280-1

7 US-10-192-280-1

7 US-10-804-408-165

US-10-804-408-165
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US-09-767-041-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                  - nucleic search, using sw model
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; Sequence 9, Application US/09767041
; Patent No. US20020055168A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Hilda
; TITLE OF INVENTION:
; FILE REFERENCE: 2183-4726
; CURRENT APPLICATION NUMBER: US/09/767,041
; CURRENT PILING DATE: 2010-10-12
; PRIOR FILING DATE: 1999-07-19
; PRIOR FILING DATE: 1999-07-19
; PRIOR PILING DATE: 1998-07-22
; PRIOR PLING DATE: 1998-07-22
; PRIOR FLING DATE: 1998-07-22
; RIOR PLING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PATENTIN VORTSION 3.0
; SEQ ID NO 9; SEQ ID NOS: 500-10 NOS: 500-10 NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO 9; SEQ ID NO
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Sequence 177,
Sequence 386,
Sequence 386,
Sequence 240,
Sequence 240,
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Sequence 302,
Sequence 174,
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US-10-329-676-18

US-10-240-453-26

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US-10-240-453-132

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US-10-231-22A-38093

US-10-808-122A-38093
3 US-10-804-408-162

3 US-11-804-408-173

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3 US-110-804-408-163

3 US-110-804-408-170

3 US-110-804-408-170

3 US-110-804-408-179

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3.2 8056 1
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CCATION: (1)..(6992)

OTHER INFORMATION: CPS 2

US-09-767-041-9
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Gaps

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Length 6992; Indels

DB 9;

Query Match
100.0%; Score 6992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6992; Conservative 0; Mismatches

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Patent No. US20020055168A1

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/767,041

CURRENT APPLICATION NUMBER: PCT/NL99/00460

PRIOR APPLICATION NUMBER: PP98202465.5

PRIOR PILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.0

SEQ ID NO 29

LENGTH: 6992
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Best Local Similarity 100.
Matches 6992; Conservative
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; OTHER INFORMATION: CPS1
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13.1 TGGTTATCTATTATCTATTTTAAATTTTATCGAAAATTTTCAACAATTTTCAACAATTTTTAAATTTTTAAATTTTTT

ATCAAGTAGAGTTTGTA 2146 |||| || || || || \ATCAGGTGGATTTTTTG 2588 CCAACAAATCGCAATCT 1546 GTGATGAGAAACCAGA 1606 3AGAAATGAAGAAGGT 1786 ||||||||||| || || 3AAGAAATGAAAAAGT 2228 ACCTCAGAATTGTCAG 2408 AAGGAAAAAAACAATTA 2086 |||||||||| AAGGGAAAAAACTATT 2528 || ||| |AGGTAAGGTTTGAAAG 1808 AATCTACATTAACTGG 1726 FIGTAACAGTAGGAACT 1846 GAAAAAAATGGAAGT 1906 TAAAAGGGACAGGTGCT 2348 TTCCAGAATATTGCAAG 1966 ACAAATCAGAAGTAGTT 2026 ragargarrigringaa 2206 | ||| || |CAGTGAATTAGAGAAT 2648 AAATGAATAATAAAA 2323 TGACTCACTTGTATTT 1426 ||||| ||||||||| || FTGTCACAGTAGGGACA 2288

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.395 TTAAGAAAGATTTATTAGTTCACAATCA----AATGACGGGGCTAATGTTTAAGTTAGA 1449
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                                                                                                                                                                                                                                                                      .035 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 1094
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     133 TATTTGAATCACATAAACAAATTCAAAAAATCTTGTTGCATTGGTAGTTTTAGGTACAG
                                       GGAATAAAT - - - ACGACCATAATTATATCGCTGTCTGTATCTTGGATTCCTCTGAAAGG
                                                                                AAATAGATAAAATTAATTTATCATTACCGCTCTATTATTCTGTGGAAGAAGCTATAGAGT
                                                                                                                    915 ATTGTTATGATTTGAAACATAACTCGTTAAGGATAATAAACAAAGATGCTCTTACTTCAG
                                                                                                                                                        553 TITCAACAAGGGAAGTGGTCGACCACGTCTTATAAATCTACCAAGTGAGTTTTTAGACG
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                                                                     APPLICANT: Miyake, Katsuhide
APPLICANT: Matanabe, Masaki
APPLICANT: Matanabe, Masaki
APPLICANT: Ijima, Shinji
TITLE OF INVENTION: Beta 1,3-galactosyltransferase and DNA encoding the
FILE REPERENCE: 766.53
CURRENT APPLICATION NUMBER: US/10/865,873
CURRENT APPLICATION NUMBER: US/09/900,038
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
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PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-01-05
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 9.1e-93;
0; Mismatches 917; Indels
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US-10-865-873-3
; Sequence 3, Application US/10865873
; Publication No. US20050064559A1
; GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (3982)..(4953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE;
; NAME/KEY: CDS
; LOCATION: (5009)..(5947)
US-10-865-873-3
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(1816)..(2262)
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(617)..(1789)
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Best Local Similarity
Matches 1389; Conservat
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LOCATION:
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                                                                                                                                                                                     Length 17276;
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                                                                                                                                                                                   Score 726.8; DB 9;
Pred. No. 1.7e-92;
0; Mismatches 902;
SOFTWARE: PatentIn version 3.1
SEQ ID NO 83
LENGTH: 17276
TYPE: DNA
TYPE: DNA
FEATURE: Streptococcus agalactiae
                                                                                                                                                                                        10.4%;
59.2%;
                                                                                                                                                                                   Query Match
Best Local Similarity 59.2
Matches 1366; Conservative
                                                                                                                    . (8207)
                                                                                                                 ; LOCATION: (7062).
; OTHER INFORMATION
US-09-870-759-83
                                                                                                    NAME/KEY: CDS
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                                                  CATTAATTTAGTGAAAAATACTTTCTTAGCTTTTCAAAATTTTTACGTGATGAGAAACCAGA
                                                                             TGTTATTATTTCATCTGGTGCGGCCGTTGCTGTCCCCTTCTTTACATCGGAAAACTATT
                                                                                                                                    TGGAGCAAAGACGATTTATATTGAAGTATTTGATCGAGTTAATAAATCTACATTAACTGG
                                                                                                                                                                                                                                                         AAAACTAGTTTATCCCGTAACAGATATTTTTATTGTTCAGTGGGAAGAAATGAAGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 83, Application US/09870759
Patent No. US2002017551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
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US-09-870-759-83
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0	RESULT 6 US-09-751-708A-83 Sequence 83, Application US/09751708A Publication No. US20030157113A1 GENERAL INFORMATION: APPLICANT: TERMAN, DAVIG S TILLE OF INVENTION: COMPOSITIONS AND METHODS FILE REFERENCE: 751708 CURRENT APPLICATION NUMBER: US/09/751,708A CURRENT APPLICATION NUMBER: US/09/751,708A CURRENT APPLICATION NUMBER: US 60/173,371 PRIOR FILING DATE: 1999-12-28 NUMBER OF EG ID NOS: 166 SEQ ID NO 83 LENGTH: 11276 TYPE: DNA ORGANISM: Streptococcus agalactiae FRATURE: NAMERIES NAMER INFORMATION: (8207) OTHER INFORMATION: US-09-751-708A-83	Query Match 10.4%; Score 726.8;
1024 AGATCCGCAAATCACAAACAGTTTCCATCTTTTCTCCAAATAGACTAGGTC 5661 904 AGAATGGCCATATTTACATTCTACAAGTTTCCATCGATGTTGATGTTGATGCTGAGGAGC 963 904 AGAATGGACGCATATTTACATTCTATACATTCCATCGATGATGCTGATGCAGACAA 5721 904 AGAATGGTAGGATTTTTAGATTCTATACATCGATGCGATAGATGCAGAACAAA 5721 904 GCAAAAAAAACAAACCAGATACAAACCAGATGCGATAGATGCAGAACAAAA 5721 904 GCAAAAAAAAACAAACCAGAAAACCAGATGCGATAGATTTAAAAAAAA	1264 TTGGTTGGATTAGCATACATTGATATTGGACTATCTGGTCAGATATTAAATTTAT	1607 TGTTATTATTCATCTGGTGCGGCCGTTGCTTCTTTTACATCGGAAACTATT 1666 1617 TGTTATTATTTCATCTGGTGCGGCCGTTGCTTCTTTTTTTATATTGGTAAGTTATT 6435 1667 TGGTGCAAACGATTTATATTGATCGACTTCTTTTTTTTTGGTAAGTTATT 6435 1667 TGGAGCAAACGATTTATATTGATCGACTTAATTGGTAAACTTACTGG 1726 1668 TGGTTGTAACCGTTAATAGAGGTTTTTATTGTTCAAGAGAAACGAAAAGAAAG
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IS FOR TREATMENT OF NEOPLASTIC DISEASE TATAGAAATATAGATGATTTGTTGAA 2206 CTCTTACATGAAGAGCTGAGATTGTT 6795 9 ATCATAATGATGGTTCATTATTTTGCAT 132 TITCITACGGCAGIAICAITITIGITGG 252 ACAATATATAACAAATCAGAAGTAGTT 2026 TCTGCAATCTTAACAAGTCATATACCAA 75 7e-92; ss 902; Indels 38; Gaps DB 10; Length 17276;

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TAAAGTTAGATGTTCAATAATCAATGAATGGTCTATTTGGTCAGATATTAAGATTATTC 6075
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            3362 AATACCAAATACAAGATATTATTAATGACATTGAAGCAATGGGAGTGATTGTCAATGTTA 5421
                                                                                         3422 ATGTAGAGGCACTTAGCTTTGATATATAGGAGAAAAGCGAATCCAAACTTTTGAAGGAT 5481
                                                                                                                                                                     ATAGTGTTATTACATATTCTATAAATTCTATAAATATAGTCACCTTATAGCAAAACGAT 5541
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Pred. No. 1.7e-92;
0; Mismatches 902; Indels
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR PAPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR PILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR PILING DATE: 2002-08-28
PRIOR FILING DATE: 2002-08-28
PRIOR FILING DATE: 2002-08-29
PRIOR FILING DATE: 2002-010
PRIOR PILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-02
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PRIOR PILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR PILING DATE: 2003-10-02
PRIOR PILING DATE: 2003-10-03
PRIOR PILING DATE: 2003-01-09
PRIOR SEQ ID NOS: 224
NUMBER OF SEQ ID NOS: 224
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Best Local Similarity 59.2%;
Matches 1366; Conservative
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; LOCATION: (7062)..(8207)
US-10-428-817A-79
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                                                          TITIATCITICICATITITACAGAGACTITIGGAGTCGTGGCTATCITGAAGAGTTTAAA
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CICCCAATITIAAAAGCAATAAAGATITATIGITIGITCTAATIGATACATIATATIGIC
                                                                                                AAAACATTTAACTATAATATATTTGCAATTTTTTCTTACGGCAGTATCATTTTTGTTG
                                                                                                                                                                GAGAATAATTTCGCACTTTCAAGACGTGGTGCCGTGTATTTCACATTAATAAACTTCGTT
                                                                                                                                                                                                                              TIGGIAIACCTAITTAACGIAATTAITAAGCAGTTIAAGGAIAGCITTCTAITTTCGACA
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TITLE OF INVENTION: STREPFOCOCCUS AGALACTIAE CAPSULAR POLYSACCHARIDE SYNTHESIS
TITLE OF INVENTION: GENES
FILE REFERENCE: 475412001300
CURRENT APPLICATION NUMBER: US/10/192,280
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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                                                                                                               TTATCCTAAGGCAATTAATTTTAGGAGGAATTTTTTAATGATTTTTGTCACAGTGGGGACA
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Pred. No. 1.1e-91;
0; Mismatches 926; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10192280; Publication No. US20040009574A1; GENERAL INFORMATION:
APPLICANT: Dattagupta, Nanibhushan; APPLICANT: Shah, Ketan
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Best Local Similarity 58.9%;
Matches 1389; Conservative C
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US-10-192-280-1
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GENERAL INFORMATION:

APPLICANT: Neetec, S.A.

APPLICANT: Neetec, Jean-Richard

APPLICANT: Neetec, Jean-Richard

APPLICANT: Mollete, B.

APPLICANT: Mollete, B.

APPLICANT: Stingele, Francesca

APPLICANT: Zinc, Robert

APPLICANT: Zinc, Robert

APPLICANT: Kratky, Zoe

ITLE OF INVENTION: Human Milk and Corresponding Genes

FILE REFERENCE: 88265-10322

CURRENT PRILION DATE: 2003-06-16

PRIOR APPLICATION NUMBER: US 09/548,606

PRIOR APPLICATION NUMBER: PT/FP 98 06636

PRIOR APPLICATION NUMBER: CT/FP 98 06636

PRIOR PILING DATE: 1998-10-09

PRIOR FILING DATE: 1998-10-09

PRIOR FILING DATE: 2000-01-01

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.2

SEQ ID NO 4

LENGTH: 18373
                              6375 GAATTTGCTCATTGCTTAAATTGTTAGGAATTCCAACGACAGTAGCTGTTGGGAATTAT 6434
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2263 TGAAAGATTAAAACAAATAGTTGAAAAATTTAATGAGGGATCAAGAAAATGAATAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptococcus macedonicus
                                                                                                                                                                                                  ; Sequence 4, Application US/10461990; Publication No. US20040023361A1; GENERAL INFORMATION:
                                                                    2323 AAGATGCATATTTGATA 2339
                                                                                                        7485 AAAAATTGAAATTAACA 7501
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US-10-461-990-4
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10099 10270 10150 10797 ATATTGTGGATAATGAGTTAATCAGTATTATTGTTCCTGTATACAATGTTGAAAAATACA 10856 10210 10271 ACTGAAGAATTACGATGGTTACCTGAGAAGTAACTGAAGTTAATATTCCAGACATAAAA 10330 10390 10391 TTGAGACTTCCTTCATTTGAGGGGAGAAGTTTTTGTCTGAAGAAATTTTTTATATTATA 10450 10684 10685 AAGAATGAAAATATTCCCCAAGAGCTATCTGTTGGGGAACGTATGCTAAAACCATTGGCA 10744 10745 TATTTATTTTATTT-----AAAAGGTATAAATAGGAATAAGTATCATAGTGGGGG 10796 5220 5280 4860 10505 TATCTAGAACATGGTCTAACTAATAATCTTTTTCATCTGTGGAAGAAGAACCCCAAGAGC 10564 10565 ACTTATTTATTGTTTAAAGAGAGAGAAAAATATATCTGCAAAATTTATCTGCAAAATTTATC TAGATGATGGCTCTGTAGATGATTCTGCTAAAATATGCAAGGAATATGCAGAAAAAGATA 5340 10625 cgaarrerigaarrerraaagrercrigaargaacaagcarrarcecragcaacarca TIGCTAAGTGTTTGGACTCTTTAGTTAACCAAACATATTTAAATATATAAAATACTTCTAA 4261 AACAGTATTATTAACCAAACATATACTAATTTAGAGGTTATTCTCGTAAATGATGGAAGT 9959 GAGTCACTAAGGAAGCAGACTTGTAAAGAGTTTATTTGGCTAATTGTCGATGATGGTTCA 10019 AATGATGGTACTG----AATTTTATATTAGACAGTTACGATCTGAATATATTTTTGATAT 10100 GGCAAACATACTGCGTATAATTTAGCTTTAGATTATATGGGAG------GAGAGGGA 10151 TGGCATATGGTTGGTAGATGATTGGTTAGCTAGCACACGCTGTTGAATGTATTATT 10211 AAAGATATCTCCTCACTTCAAGTTGGTAAGCTTGGAGTTGTATATCCAAAATATAGTTTA 4681 TATTCACGAGATATTATAAAAGATATAAAATTCCAAATTAATAGAAGTATTGGTGAG 10331 TIGAAATACGGGCITICAATCGAGACIGCAATIGITATTAAAAATITATICATIGGICAA 4741 GATTTGCTTTTTAATTTGGAGGTCTTGAACAATGTAACACGTGTAGTAGTTGATACTAGA 4801 GAATATTATTATAATTATGTCATTCGTAACAGTTCGCTTATTAATCAGAAATTCTCTATA 10451 CTATCGGAGTTTGGAAATTTTCTTCCTCTTAATAGAAGAATATAT-----TTTTTTGAA 4861 AATAATATTGATTTAGTCACAAGATTGGAGAATTACCCCTTTAAGTTAAAAAGAGAGTTT 4921 AGTCATTATTTTGATGCAAAAGTTATTAAAGAGAAGGTTAAATGTTTAAACAAAATGTAT 4981 TCAACAGATTGTTTGGATAATGAGTTCTTGCCAATATTAGAGTCTTATCGAAAAGAAATA CGTAGATATCCATTTAATAAAGCGAAAAGATATTTATCAAGAAAGCATTTAGTTACGTTG TATITIGATGAAATTTTCGCCTAAACTATATGTAATGTTATAAGAAATTTCAAAAGCAG 5161 TAGAGGTAAAAATGGATAAAATTAGTGTTATTGTTCCAGTTTATAATGTAGATAAATATT 5221 TAAGTAGTTGTATAGAAAGCATTATTAATCAAAATTATAAAAATATAGAAATATTGA 4381 TACAAGAAATTAATGGCGGTCTAGCAGATGCTCGAAATTTCGGACTAGAACATGCAACA 4561 GACGAAAACGGGTATACAAAGAAAAAAAAAATAGTAATTTTTCATGTCTTAACGAGAGAA 4321 ACTGATGATTCTGAGAAATTTGCTTAAACTATATGAAGAACGATGGAAGAATTAAATAT 4441 GGTAAATATTGCTTTTGTCGATTCTGATGACTATATAGAAGTTGCAATGTTCGAGAGA 4621 GAGACTGTAAAAGAATTTTTGTCAGGATCTAATATAGAAAATAATGTTTGGTGCAAGCTT 5041 5101 5281

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                                                                                                               AAAGAGTAAAAATTTTTTCACTAATCATAGTGGAGTATCAAATGCTAGAAATCATGGAA
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Sequence 166, Application US/10804408 Publication No. US20040253617A1 GENERAL INFORMATION:

RESULT 10 US-10-804-408-166 APPLICANT: FANRONG, KONG

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APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B STREPTOCOCCI
FILE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
FRIOR APPLICATION NUMBER: PCT/AU02/01281
FRIOR FILING DATE: 2002-09-18
FRIOR FILING DATE: 2002-09-18
FRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SSOFTWARE: Patentin version 3.2
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Pred. No. 2.6e-82;
0; Mismatches 791; Indels
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Best Local Similarity
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	167, Application US/10804408 167, Application US/10804408 INFORMATION: WT: PANRONG, KONG WT: GILBERT, GWENDOLIN WT: GILBERT, GWENDOLIN FILNGTON: 675002-2001 FILING DATE: 2004-03-19 PPLICATION NUMBER: BCT/AU02/01281 ILING DATE: 2002-09-18 PPLICATION NUMBER: PCT/AU02/01281 ILING DATE: 2002-09-18 PPLICATION NUMBER: AU PR 7749 ILING DATE: 2001-09-19 PPLICATION NUMBER: AU PR 7749 ILING DATE: 2001-09-19 PROBLE 2001-09-19 SE PATENTIN VERSION 3.2 167 : 2226 3N: Streptococcus agalactiae 408-167	Similarity 59.6%; Pred. No. 2. 6e-82; Conservative 0; Mismatches 791; Indels TGGCATTATTGATATGATAGGATTTTTTTTTTTTTTTTT
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Pred. No. 4.3e-82;
0; Mismatches 792; Indels
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APPLICANT: GILBERT, GWENDOLYN
ITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S;
FILE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT RILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR PILING DATE: 2002-09-18
PRIOR PILING DATE: 2001-09-19
NUMBER: OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SEQ ID NO 162
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                                                                                                                                      Score 649.2; DB 18; Length
Pred. No. 7.3e-82;
0; Mismatches 793; Indels
                                                                                                    OTHER INFORMATION: Consensus sequence
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 2226
                                                                                                                                      Query Match
Best Local Similarity 59.5%;
Matches 1223; Conservative (
                                                                              ORGANISM: Artificial Sequence
                                                                                                         ; OTHER INFORMA
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                      GATCAAGCTTTTATTAACATACCATTGAATTATTTGGTA 778
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GACCACGICTITATAAAICTACCAAGTGAGTITTTAG--- 609
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353 AGAITATTCATTTTCATATTTTCATATTTCATATTTTTTTTT		473 TATTGTATCTATTGAATTTTTAAAATATTATCGAAAATATTTTGCTAAGATTTT 532	373 TCTATCAAAAAAGACGATTCTAATTACAACGGCTGAACGATGGGAAAAATATGCAAGTTT 432	433 TATTIGAAICACATAAACAAATICAAAAAAAICTIGITGCATIGGIAGTITIAGGIACAG 492 	493 AAATAGATAAAATTAATTTATCGGTTCTATTATTCTGTGGAAGAAGCTATAGAGT 552 	553 TITCAACAAGGGAAGTGGTCGACCACGTCTITATAAATCTACCAAGTGAGTTTTTAG 609 110 AGTTAACCTGCTTAAACATCAAGCKTTTATTAACATACCCATTGAATTATTGGTA 769	610ACGTAAAAGCAATTCGTTTCAGATTTTGAGTTGTTAGGTATTGATGTAAGGTTG 663 	664 ATATTAATTCGGTTTTACTGCGTTGAAAAACAAAAATCCAACTGCTAGGTGACC 723 	724 ATAGCATTGTAACTTTTTCCACAAATTTTTATAAGCCTAGTCATATCATGATGAAACGAC 783 	784 ITTTGGATATACTCGGAGGGTAGTCGGGTTAALTATTTGTGGTATAGTTTCTATTTTGT 843	844 TAGITICCAAITAITEGIAGAIGGIAGACGGCTAITITIGCTCAGAAACGAGTIGGAC 903 	904 AGAATGGACGCAFATTTACATTCTACAAGTTTCGATGTATGTTGATGCTGAGGAGC 963 	964 GCAAAAAAGACTIGGICAGCCAAAACCAGAIGCAAGGGIGGGTATGITITAAAATGGGAA 1023 	1024 AAACGATCCTAGAATTACTCCAATTGGACATTTCATACGCAAAACAAGTTTAGACGAGT 1083 	1084 TACCACAGITITATAATGITITAATIGGCGATATGAGTCTAGTIGGTACACGTCCACCTA 1143	1144 CAGTICAIGAATITICAAAAAITATACTICCTGGTCAAAGAGACGATTGAGTTTTAAACCAG 1203 	1204 GGATTACAGGICTCTGGCAGGTTAGTGGTCGTAGTAATATCACAGACTTCGACGACGTAG 1263 	1264 TTCGGTTGGACTTAGCATACATTGATAATTGGACTATCTGGTCAGATATTAAAATTTAT 1323
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                         APPLICANT: FANKONG, KONG
APPLICANT: FANKONG, KONG
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B STREPTOCOCCI
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B STREPTOCOCCI
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-09-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR FILING DATE: 2002-09-18
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
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0; Mismatches 794; Indels
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
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Pred. No. 1.2e-81;
0; Mismatches 794; Indels
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                                                                                                                                           GROUP
Sequence 169, Application US/10804408
Publication No. US20040253617A1
GENERAL INPORMATION:
APPLICANT: FAMENOG, KONG
APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: WOLECULAR TYPING OF GROUN
FILLE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
FILLS PRIOR APPLICATION NUMBER: DCT/AU02/01281
PRIOR FILLING DATE: 2002-09-18
PRIOR FILLING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
SEQ ID NO 169
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Pred. No. 2e-81;
0; Mismatches 795;
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Publication No. US20040253617A1

GENERAL INFORMATION:

APPLICANT: FANRONG, KONG

APPLICANT: FANRONG, KONG

TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S;

FILE REFERENCE: 675002-2001

CURRENT FILING DATE: 2004-03-19

FRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 182

SEQ ID NO 164

LENGTH: 2217
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Publication No. US20040253617A1
GENERAL INFORMATION;
JAPPLICANT: FANRONG, KONG
APPLICANT: FANRONG, KONG
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S'
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S'
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT APPLICATION NUMBER: DCT/AU02/01281
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR FILING DATE: 2000-09-18
NUMBER: OF SEQ ID NOS: 182
SOFTWARE: PALENTIN VENSION 3.2
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                 APPLICANT: FANENCY, KONG
APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROUP B S;
FILE REFERENCE: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR PILING DATE: 2002-09-18
PRIOR PLING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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Pred. No. 3.4e-81
                                                                                                                                                                                      ORGANISM: Streptococcus agalactiae
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 US20040253617A1
                                                                                                                                                                                                                                    Best Local Similarity 59.4
Matches 1220; Conservative
Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                 53 TTTCAACAAGGGAAGTGGTCGACCACGTCTTTATAAATCTACCAAGTGAGTTTTTAG---
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Pred. No. 2.1e-80;
0; Mismatches 792; Indels
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APPLICANT: FAURONG, MOLECULAR TYPING OF GROUF
TITLE OF INVENTION: MOLECULAR TYPING OF GROUF
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/ANU2/01281
PRIOR PILING DATE: 2002-09-18
PRIOR PLING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
SPRIOR FILING DATE: 2001-09-19
SPRIOR FILING DATE: 2001-09-19
SPRIOR FILING DATE: 2001-09-19
SPRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PATENTIN VETSION 3.2
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Publication No. US20040253617A1
GENERAL INFORMATION:
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Best Local Similarity 59.5%;
Matches 1223; Conservative
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Pred. No. 1.3e-50;
0; Mismatches 581;
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Best Local Similarity 58.9<sup>1</sup>
Matches 849; Conservative
      CDS (1809)..(2501)
                                                                                                                        (2618)..(3307)
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1487 AAGAAGTCTTTTGAAGAATGAAAAATGTATCCATGTTACTTTCCAACAAATCGCAATCT 1546
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                                                     1672 TAGGAGTATTCTAAGAGAGATGTTGTATATCATTGCTTCTTTCCAACAAACGTAATGT
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Biopolymer Thickner
FILE REFERENCE: 64376
CURRENT APPLICATION NUMBER: US/10/182,960
CURRENT APPLICATION NUMBER: PCT/US01/03404
PRIOR PILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-02
PRIOR FILING DATE: 2000-02-02
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LOCATION: (1020)..(1796)
FEATURE:
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NAME/KEY: CDS
LOCATION: (174)...(488)
FEATURE:
NAME/KEY: CDS
LOCATION: (528)...(977)
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SEQ ID NO 1
LENGTH: 6850
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US-10-182-960-1
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-010-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2011-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWAREE FREEEE for Windows Version 4.0
SOFTWAREE FREEEE
                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae
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58.6%;
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Matches 794; Conservative
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US-09-815-242-9587
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LOCATION: (1).
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     1229 AAAATACTTAGAAAAGAAAAACCAGATTTGATTATTTCGAGTGGTGCTGCGGTAGCCGTT 4288
                                      CCCTTCTTTACATCGGAAAACTATTTGGAGCAAAGACGATTTATATTGAAGTATTTGAT 1700
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APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari L.

APPLICANT: Oblsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Ammancto, Robert T.

APPLICANT: Yu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23
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       Length 1368;
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Score 423.2; DB 9;
Pred. No. 4.1e-50;
0; Mismatches 548;
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              GACTITITCTACAACATITIATAAAGACTAGTCATGTAATTGCTAAGCGGATTATTGATAT
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Pred. No. 1.6e-49;
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APPLICANT: GILBERT, GWENDOLNN
TITLE OF INVENTION: MOLECULAR TYPING OF GROUJ
CURRENT FILE REFERENCE: 675002-2001
CURRENT FILING DATE: 2004-03-19
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR APPLICATION NUMBER: AU PR 7749
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 178, Application US/10804408
Publication No. US20040253617A1
GENERAL INFORMATION:
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ORGANISM: Streptococcus agalactiae
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Best Local Similarity 51.9%;
Matches 1100; Conservative
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US-10-804-408-178
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US-10-804-408-178
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672 ATTAGAGGTACTCAAGAGGATATAACGTTTCAGCGATTTATTGCTGAGCTATTAAAACTA
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Pred. No. 8.9e-45;
0; Mismatches 975;
                                                                                                                            OF GROUP
                                                                                            APPLICANT: GILBERT, GWENDOLYN
TITLE OF INVENTION: MOLECULAR TYPING OF GROU
FILE REFRENCES: 675002-2001
CURRENT APPLICATION NUMBER: US/10/804,408
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: PCT/AU02/01281
PRIOR PILING DATE: 2002-09-18
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn version 3.2
LENGTH: 2577
Sequence 179, Application US/10804408
Publication No. US20040253617A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%;
Best Local Similarity 51.6%;
Matches 1092; Conservative
                                                                            KONG
                       Publication No. US20
GENERAL INFORMATION:
                                                                          APPLICANT: FANRONG,
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search completed: April 29, 2005, 01:43:00
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

April 29, 2005, 00:00:53 ; Search time 19328 Seconds (without alignments) 13769.939 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-767-041-9 6992 1 atcgccaaacgaaattggca.........gcaaacagcaaaagaagctt 6992

IDENTITY NUC Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b_est1:; 9b_htc::*; 9b_est3:*; 9b_est4::*; 9b_est6::*; 9b_9s81:*; 9b_9s81:*; EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result			1	å	ŕ	
NO.	o. score		watcn rengtn us	90	nt	Description
υ	1 169.6	5 2.4	1896	6	CG753083	CG753083 P048-1-C0
	2 167.4	4 2.4	1896	6	CG753083	CG753083 P048-1-C0
υ	3 166.4	N	1592	0	CG750135	CG750135 P044-3-D0
	4 158	8 2.3	1348	σ	CG749499	CG749499 P043-4-A0
υ	5 155.4	4 2.2	1626	7	CF238805	CF238805 AGENCOURT
	6 155	5 2.2	1392	9	CG757503	CG757503 P052-4-C0
	7 153.6	2.2	1542	σ	AG386981	AG386981 Mus muscu
	8 150.8	8 2.2	1758	.σ	CL509408	CL509408 SAIL 811
υ	9 149.6	6 2.1	1758	σ	CL509408	CL509408 SAIL_811_
_	148.2	2 2.1	1780	6	AG320553	AG320553 Mus muscu
Ü	11 146.6	6 2.1	1489	σ	AG350139	AG350139 Mus muscu
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_	144	4 2.1	1592	σ	CG750135	CG750135 P044-3-D0
Ü	14 143.4	4 2.1	1539	σ	AG340947	AG340947 Mus muscu
П	15 143.3	2 2.0	1242	σ	CL068807	CL068807 CH216-115
Ü	143	3 2.0	2015	σ	AG311015	AG311015 Mus muscu
_	17 143	3 2.0	2157	σ	CL081966	CL081966 CH216-165
-	142.6	6 . 2.0	1594	σ	CL110653	CL110653 ISB1-53P2
Ü	140.8	8 2.0	1608	σ	CL118721	CL118721 ISB1-72J8
U	20 140	0 2.0	1101	σ	CNSOOEVL	AL069706 Drosophil
Ü	21 139.8	8 2.0	1780	σ	AG320553	AG320553 Mus muscu
Ü		6 2.0	1313	7	CK997149	CK997149 ip15c02.b
υ	23 138.2	2 2.0	1745	σ	AG338221	AG338221 Mus muscu
υ	24 137.8	2.0	1943	0	AG333983	AG333983 Mus muscu

CL082000 CH216-165	AG350209 Mus muscu		AL061936 Drosophil		CC253231 CH261-180	CG749499 P043-4-A0		AG340947 Mus muscu		CG757539 P052-4-E0				AG333887 Mus muscu	CL038406 CH216-46A	CG757503 P052-4-C0	CL466243 SAIL 1253	CL466243 SAIL_1253	CL055132 CH216-80J	CL118721 ISB1-72J8
CL082000	AG350209	CG757970	CNS0021J	CL080711	CC253231	CG749499	AG386981	AG340947	CG744717	CG757539	AG430010	AG346840	AG288305	AG333887	CL038406	CG757503	CL466243	CL466243	CL055132	CL118721
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ALIGNMENTS

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        CCGACGACAATATTTATTCAAACAGGATATTCTGACTATATTCCAGAATATTGCAAGTATA 1970
                          ATTNATATAAAATTAAAAATNTAAATTATATATANAATAAATTAAAAATAAATAAATA 1646
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Neodiplogasteridae; Pristionchus.
Loases I to 1896)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental Biology
Telli 00497071601371
Fax: 00497071601498
Email: ralf:sommer@tuebingen.mpg.de
Class: BAC ends.
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the genomic DNA with EcoRI and cloning into the vector."
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Best Local Similarity 46.8%;
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Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1592)
Sinivasan, J., Sinz, W. Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1348)
Srinivasan,J., Sinz,M., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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P043-4-A06.za Ppa ECORI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
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                                                                                                                                 pacificus"
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
                                                                                                    1. .1592
/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      2.4%;
ilarity 43.1%;
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/organism="Pristionchus pacificus"
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/strāin="california"
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                                                                                                                                     Gaps
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Pred. No. 3e-14;
0; Mismatches 631; Indels 15;
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ilarity 47.1%;
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/lab host="DH10B (phage-resistant)"
/clone lib="NIGHD XGC Emb6"
/note="Vector: pCMV-SPORT6.1; Site 1: Not1; Site 2: EcoRV;
cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC): library.
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Conteact: Deniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert M. Grainger
Tissue Procurement: Robert M. Grainger
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14680 row: g column: 21
High quality sequence statt: 71
High quality sequence stop: 316.
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AGENCOURT 15099447 NICHD_XGC_Emb6 Xenopus tropicalis cDNA clone
IMAGE:6995950 5', mRNA sequence.
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1 (bases 1 to 1626)
11H-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea,
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    .1626
    /organism="Xenopus tropicalis"

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/clone="IMAGE:6995950"
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Query Match 2.2%; Score 155.4; DB 7; Length 1626; Best Local Similarity 42.5%; Pred. No. 7.5e-14; Matches 665; Conservative 0; Mismatches 885; Indels 15; Gaps 2; 2709 TGATTTTGTGGCAATTCTTTAAAAAAAAAAAAAAAAAAA	2769 TAAATGTCCAGATGAACTATTTATACAGACAATTATAGAAAAATATGAATTTGAAATAG 2828 		2949 IGCTAGAAAGTTAAAAATAGAAATAAATTTAAAGTAATTTATTA	3069 TTTATTITTAAGIACTTCGTTGATTATTTTATTCCAGAGCAAAGTATGTTTTTAT 3128 1255 TTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AGIACTTIGTIGAAATAATTTIGAAAGATTATTTGCTGCTCCCATAATT	3669 TCGTAGCAATATTATTATATGCTTGTTATGGGAGATATATAGGTGGAAAATTTGCTTGG 3728
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, Wiggers-Perebolte,L., Jansen,K., ad Sommer,R.J. AGAGAATCAAGTAACGAAGCTAGATTTATT 3848 GGAAGTCATTCAGGCTATATATCATTTTT 3968 ACTGATGTTTTTTTTTTATGTTATAAA 4028 CTACTTATTTTTAAATACTGAATTGCTT 3788 GAAAACAATATTTATTTGGATATGGAATA 3908 CTATITITITITACATCATTAGCCATATIT 4088 SGATATGGAGACAAAAATGAATGATTTAAT 4208 ATTATATATAGTACTATTCTTTCTTCAATA 4148 DNA linear GSS 24-OCT-2003 rary Pristionchus pacificus genomic, TATATATATATATATATATATATATA 251 MNNNAAAAAATATTTATAAATTTTTTTT 551 AATTÄÄAATTTTTTTTTTTTTTTTTTT 491 romadorea; Diplogasterida; mental Biology 2076, Germany 5-722 (2003) pacificus" de.

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        /db_xref="taxon:54126"
/clone_lib="tpa EcoR! BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoR! and cloning into the BAC
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Pred. No. 8.7e-14;
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Pel:81-45-503-911, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSWG01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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Mus musculus molossinus DNA, clone:MSMg01-201G10.TJ, genomic survey
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1238 ATTTTTTTTTTTTATTATAAAIATTATTATTATTATTTATTTATATTANTTATTTTTTT
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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/organism="Mus musculus molossinus"
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sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMg01-201G10.TJ"

/sex="male"
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BAC end Sequences of Library MSMg01
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                                                                                                                                             3738 CTAATAGTAATATTTGTAATACTACTTATTATTTTAAATACTGAATTGCTTTACCATGAA 3797
                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 chases I to 1788)
1 chases I to 1788)
26sssions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J. D., Cotton, D., Misch, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
                                                                                                                                                                                                                                                                                                                                  CL509408
SAIL_811 H11.v3 SAIL Collection Arabidopsis thaliana genomic clone CL509408.
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Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Syngenta Biotechnology Inc.
Bmail: allen. Sessions@Syngenta.com
ABRC Stock Number CS836276; T-DNA left border flanking sequences of Syngenta Arabidopsis Insertion Library (SAIL) lines are available syngenta Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
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/clone=11b="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
                                                  3618 TGTCTTGCTTTTATACCGATCTATTTAAGTGGATCGAGAATTGGTAGTTTATCGCTAGCA
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Pred. No. 3.7e-13;
0; Mismatches 1084;
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/mol_type="genomic DNA"
/ecotype="Columbia"
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                                                                Length 1542;
/tissue_type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"
                                                                           Pred. No. 1.4e-13;
0; Mismatches 664; Indels
                                                                DB 9;
                                                                Score 153.6;
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2028 TITGCCACGGGGCCCCGCTACTITTATGAATTCATTATCCAAGGAAAAAAAAAA	2688 TAATTGGGTTTCGCTTCCACATGATTTTGTGGCAATTCTTTATCAAATGAAAACGAAAC 2747 736 NAWNNAAAAAAAAAANANAAANNAAANAAAAAAAAAAA
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yngenta.com –
276; T-DNA left border flanking sequences of
sertion Library (SAIL) lines are available
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llection Arabidopsis thaliana genomic clone
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assicales; Brassicaceae; Arabidopsis.
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AG320553 1780 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-106H14.TJ, genomic survey
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through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and single contiguous sequences.

Class: Thom tagged.

Location/Qualifiers
                                                                                                                                    isolated
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                                                                                                                                                                             2.1%; Score 149.6; DB 9; Length 1758; Similarity 36.2%; Pred. No. 5.7e-13; Conservative 0; Mismatches 1086; Indels 27;
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                                                                                                /db_xrefe="taxon:3702"
/clone="SAIL 811 H11.v3"
/clone=1ib="SAIL Collection"
/note="T-DNA left border sequences"
modified TAIL-PCR strategy"
                                                                   organism="Arabidopsis thaliana"
                                                                               /mol_type="genomic DNA"
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                                                                                                                                                                           Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Conter (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3246 ACAAGTATGTTTGTTGAAATAAATTTTGAAAGATTATTTGCAGATTTTACTGCTCCCATA 3305
                                                                                                                                                                                                                                                      MSMg01. For BAC
be (abe@rtc.riken.jp)
                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                              and Chemical Research (RIKEN), Genomic Sciences Center (SSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Ja (E-mail:hattori@gec.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken. Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                      Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
                                                                                                                                                         Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="mixture of kidney and spleen"`
/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Mus musculus molossinus"
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.larity 47.2%; Pred. No. 9.3e-13;
Conservative 0; Mismatches 776;
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/sub_species="molossinus"
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/sex="male"
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1. .1780
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                                       musculus molossinus
musculus molossinus
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S Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission

Linect Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

17-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9199
                                                                                                                                            AG350139 1489 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-146K14.TJ, genomic survey
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TTATGAATTCATTATCCAAAGGAAAAAAAAATTATTGTTTCCTAGACAAAAAAAGTATG 2111
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BAC end Sequences of Library MSMg01
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 1.7e-12;
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/clone="MSMg01-146K14.TJ"
/sex="male"
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/sub_species="molossinus"
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Mus musculus molossinus
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                                                                                                                      AG350139 1489 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-146K14.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                         Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chout, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gec.riken.ip, URL:http://hgp.gec.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170; //hgp.gec.riken.go.jp/, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
                                                                                                                                                                                                                                                                              Noguchi, H., Kojima, T. and Sakaki, Y.
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clone lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 3.6e-12;
0; Mismatches 699;
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BAC end Sequences of Library MSMg01
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/sub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:57486"
/clone="MSMg01-146K14.TJ"
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                                        Mus musculus molossinus
Mus musculus molossinus
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                        3371 AAAAATAGTATCTTTT
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Neodiplogasteridae; Pristionchus.
1 (bases I to 1592)
2 Krinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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1371 TAATTTACANTATATTATATAATAATATTTATATTANCATTTATAATATTAATNTATA 1430
                                                                                                                      CG750135 1592 bp DNA linear GSS 24-OCT-2003 P044-3-D09.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
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/clone lib="pa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
                                                  TTTATTAGGTATATCTGCATTGTATATTATTCAAAATGGGAAAGATATTGTATTTT
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Pred. No. 4.1e-12;
0; Mismatches 810; Indels
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Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .1592
/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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CG750135
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                                                                                                                                                                                                                                                                                and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorieges.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:B1-45-503-9111, Fax:s1-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba 305-0074 Japan Phone: B1-298-36-9189, fax: B1-298-36-9199
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                           1539 bp DNA linear GSS 02-JUN-2004 molossinus DNA, clone:MSMg01-134C16.T7, genomic survey
                                                                                                                                                                                                                                                                     Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                   Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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larity 45.5%; Pred. No. 5.1e-12;
Conservative 0; Mismatches 733;
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    1539
    /organism="Mus musculus mc/mol_type="genomic DNA"
    /sub_species="molossinus"

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/clone="MSMg01-134C16.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                               musculus molossinus
                                                                                  GI:47914257
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2015 bp DNA linear GSS 02-JUN-2004 molossinus DNA, clone:MSMg01-093J24.TJ, genomic survey
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 2015)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1242)
Mardis,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 7
High quality sequence stop: 57.
Location/Qualifiers
                                                                                                                                                                      Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-115B3"
                                                                                                    CH216-115B3, genomic survey sequence.
                                                                  CL068807 1242 bp
CH216-115B3_Sp6.1 CH216 Xenopus
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      Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mall-hattori@gsc.riken.ip, WL.http://hgp.gsc.riken.go.jp/, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199
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'clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                       Score 143; DB 9; Length 20
Pred. No. 5.7e-12;
0; Mismatches 880; Indels
                                                                                                                                                                                                                             organism="Mus musculus molossinus"
                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                       clone="MSMg01-093J24.TJ"
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3429 3488 3548 3608 3665 3844 3964 4024 4084 4144 4204 3845 TATTATTTATCAAGGAAGTATTGATAAAGTATTAGAAAACAATATTTTATTTGGATATGG 3904 TTATCGCTAGCAATATTAATTATATGCTTGTTATGGAGATATAT-AGGTGGAAATTTGC 3724 TTGGATAAAAAAGCTAATAGTAATATTTGTAATACTACTTATTTTTTAAATACTGAATT 3784 609 199 849 551 491 434 314 **AAAATGAAATTTTATTGTTTTTATTATGGTCTATATTATGTTTTGTTTTCAGTAGTCACAA** 3370 TAAAAAATAGTATCTTTTTTAGTTTTTTAGTTTTAGTTATATGTTATCTGCATTGTATATTA TTTTTCTTGTGTCTTTGTATACCGATCTATTTAAGTGGATCGAGA---ATTGGTAGT 1666116NTACTTTTTTTTTTTTTTTTTTAGATACTTATAGAGATAGTAGTATTTTTTT 3785 GCTTTACCATGAAATTTTGGCTGTTTATAATTCTAGAGAATCAAGTAACGAAGCTAGATT 313 ATTTTTTTTTTTGG-----TTTATTTTTTTTTTTTTTTATTTTAATTATTTTTATTTA **ATTTTTTATTATTATATATATAAAATATATAGTGGGTGNNANNNAAAGGAGTTTTTT TAATTTTTATGAATTTTAATTTTTATTTTAAAATTTTTTGAAAACTAAGCTAATATTAA** ATTITITAGITITICTAATTITIATATT ----TATATTGATTITTCTTATTTTATCTTTT GTATGTTTGTTGAAATAAATTTTGAAAGATTATTTGCAGATTTTACTGCTCCCATAATTT GGATTATTGCAATAATGTATTATAATTTGTATTCATTTATAAATATTGATTATAAAAAT ATAACAGGCGTCAAAACAAGGTTGGTTGGCTTTATGAACTATCCTACGTTAAATACCACT ATTITITITATCIAAATTITATTITTT--TICITTATTTTTTATTATTATATA cgirirarrarararrirrrrrarararraagracacarra - - rararrarrir 4025 AAAAAAAAGTTATGGAGTTAATGGGGAAACAGCACTATTTTATTTTACATCATTAGCCAT **ATTITICATATATAGAACAATAGATCCGATTATTATTATTATTAGTACTATTCTTTTCTTC**

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3529 ATCCTACGTTAAATACCACTACAATTATAGTTTCAATTCCGTTAATCTTTGCACTTATAA 3588
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1289 ATTTTACTGCTCCCATAATTTGGATTATTGCAATAATGTATTATAATTTGTATTCATTTA
                                                            TAAATATTGATTATAAAAATTAAAAATAGTATCTTTTTTAGTTTTTAGTTTTTATTAG
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Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butamphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 2157)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agaaaaggttttttttttttttttttgggagnaaaagaaannaanagaggatagga
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                                                                                                                      CL081966 2157 bp DNA linear GSS 3:
CH216-165D13_Sp5.1 CH216 Xenopus tropicalis genomic clone
CH216-165D13, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
                                                                                                                                                                                                                     Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Xenopus tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: Sp5 atctgccgtttcgatcct
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence start: 341 quality sequence stop: 412. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-165D13"
                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard K Wilson
                                                                                                                                                                                    CL081966.1 GI:40537879
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AUTHORS
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CL118721 168 bp DNA linear GSS 05-JAN-2004 ISB1-7248 T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-7278, genomic survey sequence. CL118721
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Xenopus tropicalis (western clawed frog)
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1 (bases 1 to 1594)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Aphysical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC
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Library Segment 1"
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Pred. No. 6.7e-12;
0; Mismatches 729;
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Washington University School of Medicine
                                                                                                                                     Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                         Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                      Class: BAC ends
High quality sequence start: 390
High quality sequence stop: 470.
Location/Qualifiers
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clone="ISB1-53P23"
clone lib="ISB1"
                                                                                                                                                                                                                                                                                          Contact: Richard K Wilson
                                                                             genomic survey sequence.
                                                                                                      CL110653.1 GI:40604288
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Best Local Similarity 45.2%;
Matches 608; Conservative
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                            Tritiatatititatatititatatititititititatatatatatitititatatitit
                                                                                                                  3432 CAAAATGGGAAAGATATTGTATTTTTAGACAGACACCTTATAGGACTAGACTATCTTATA
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                                                                                      ACAGGCGTCAAAACAAGGTTGGTTGGCTTTATGAACTATCCTACGTTAAATACCACTACA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Maphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,

Xenopodinae, Xenopus, Silurana.

1 (bases 1 to 1608)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"
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Pred. No. 1.3e-11;
0; Mismatches 792; Indels
                                                                                                                                         Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 252
High quality sequence stop: 345.
                                                                                                                                                                                                                                                                      1. .1608
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db xref="taxon:8364"
/clone="1SB1-7238"
                                                                                                                                                                                                                                                                                                                                          /clone lib="ISB1
                                                                                                                             Contact: Richard K Wilson
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29923 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALO69706.1 GI:4949849
                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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To Chaese 1 to 1780)

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

[E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Faz:81-45-503-9170)

Clones are derived from the mouse BAC library MSMOIL For BAC
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                                                                                                                                                                                                                                                             AG320553 1780 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-106H14.TJ, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Kuniya Abe (abe@rtc.riken.jp)
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                        2802 TATAGAAAATATGAATTTTCAAATAGATTATCTAAATATGGAAATTTAAGATATATAAA
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BAC end Sequences of Library MSMg01
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/clone_lib="MSMg01 Mouse Male BAC Library"
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/sub_species="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                       - Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila denome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3027 GAGTAATGTATGTTTAAATTATTTAAATATGACCCGGAATATTTTTATTTTTAAGTACTTC 3086
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                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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TOAWATTTTTWWIMTATTTWATWWTATWITWWT
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:7227"
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note="end : T7"
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/clone_lib="RPCI-98
                                                                                              Direct Submission
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/dome lib-"Brain - Cerebellum Library (DOGEST8)"
/clone lib-"Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site_1:
CoRI; Site_2: Xhoi; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6651"
                                                                                                                                                                                                                                                                                                                                                                             1313 bp mRNA linear EST 26-MAR-2004 ipl5c02.bl Brain - Cerebellum Library (DOGESTE) Canis familiaris CENA clone ipl5c02, mRNA sequence.
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                                                                     1110 CCGATTATTATTATATTAGTACTATTCTTTCTTCAATAGGTATTTGGAATAATATAAAT 4169
                                                                                                                                         1170 TTTAAAAAGGATATGGAGACAAAAATGAATGATTTAATTTTCAGTTATTGTACCAATTTA 4229
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                       050 GAAACAGCACTATTTTATTTTACATCATTAGCCATATTTTTCATATATGAAACAATAGAT
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/dev stage="3 month old normal canine"
/lab_host="XL10 Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: W. Richard McCombie
Cold Spring Hazen Genome Sequencing Center
Cold Spring Hazbor Labbratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tal: 516 367 8884
Pax: 516 367 8884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Balija,V., Nascimento,L.U. and McCombie,W.R. ESTs from Canis familiaris cerebellum (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%; Score 138.6; DB 7;
.larity 48.5%; Pred. No. 2.8e-11;
Conservative 0; Mismatches 580;

    1313
    organism="Canis familiaris"

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Plate: ipl5 row. c column: 02
High quality sequence stop: 1313
Location/Qualifiers
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/db_xref="taxon:9615"
/clone="ip15c02"
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Canis familiaris
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Matches 567;
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                                                 1600 ATTTÄTÄGAGTATÄCTÄTATÄTÄÄÄÄTÄTÄATAATAATÄTTTTTTATÄTÄÄTTATTÄTT 1541
                                                                                                                     ATTCCAGAGCAAAAGTATGTATTTTATTAATTTTTATGAATTTAATTTTATTTCATATA 3161
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gec.riken.jb, With.http://hgp.gsc.riken.go.jb/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone; 81-298-36-9189, fax: 81-298-36-9199
                                                                                                        AG338221 1745 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-130H15.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2344 CTTATCATAATTTTTCTCAGATTTTACTGGAGAGGGATACAGATATTATCATCTTCTCTC 2403
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2224 TAAGCAAACTAACTTTACATCAAATAATAATTTTTTTTTGTGAAAGATTAAAAACAAATAGT
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                                                                                                                                                                                                                                                                                                                                         Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                           Kojima, T. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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/organism="Mus musculus molossinus"
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Pred. No. 3.1e-11;
0; Mismatches 643;
3856 AAGGAAGTATTGATAAAGTATTAGAAACA 3885
                              157
                                                                                                                                                                                                                                                                          Hattori,M., Toyoda,A., Noguchi,H., 1
BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                   Mus musculus molossinus
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musculus molossinus DNA, clone:MSMg01-124L03.T7, genomic survey
                                                                                                                                                                                                                                                               Submitted (17-NOW-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOW-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel:81-45-503-9111, Fax:81-45-503-9170; //hgp.gsc.riken.go.jp/, Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1791 TATAATAATATTGTATTTATATATCATÄTTGCAAAATACATAGATTTATTATAAT 1732
                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                     Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
                                                                                                                                                                    Kojima, T. and Sakaki, Y.
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45.7%; Pred. No. 3.6e-11;
iive 0; Mismatches 947;
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BAC end Sequences of Library MSMg01
Unpublished
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-124L03.T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            .: abe@rtc.riken.jp
                                                                                  Mus musculus molossinus
Mus musculus molossinus
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CH216-165P18_RM4.1 CH216 Xenopus tropicalis genomic clone CH216-165P18, genomic survey sequence. CL082000
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3519 ITTAIGAACTAICCIACGITAAAIACCACTACAATTATAGITICAAITCCGITAAICTIT 3578
                                                            3579 GCACTTATAAAAAATAAAATGCAACAATTTTTTTTTTCTTGTGTCTTGCTTTTATACCGATC 3638
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Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
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Class: BAC ends
High quality sequence start: 265
High quality sequence stop: 497.
Location/Qualifiers
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/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-165P18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Richard K Wilson
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GSS.
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Best Local Similarity 43.4%;
Matches 674; Conservative
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/cell line='
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1981)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Andráis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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Pred. No. 3.8e-11;
0; Mismatches 876;
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à	4011	TTTTTTTATGTTATAAAAAAGTTATGGAGTTAATGGGGAAACAGCACTATTTTATTTT 4	4070
qq	1285		1344
ò	4071	ACATCATTAGCCATATTTTTCATATAGAACAATAGATCCGATTATTATTATTATTAGTA 4	4130
qq	1345	TATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1404
à	4131	CTATTCTTTTCTTCAATAGGTATTTGGAATAATATAAAATTTTTAAAAAGGATATGGAGACA 4	4190
qa	1405	TATTITGTTATTATTATTATTATTTTTTTTTTTTTTTTT	1461
λ	4191	AAAAATGAATGATTTAATTTCAGTTATTGTACCAAATTTATAATGTCCAAGATTATCTTGA 4	4250
qo	1462	TTTTTARGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1521
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